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Perfect score:
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/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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10 US-09-864-761-31616

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US-09-910-943-287
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                    Sequence 7775, Ap
Sequence 161, App
Sequence 357, Appl
Sequence 3533, Ap
Sequence 3537, Ap
Sequence 1704, Ap
Sequence 1051, Ap
Sequence 31616, A
Sequence 317, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 17, Appl
Sequence 76, Appl
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Sequence 353, App Sequence 3, Appli	15, <i>1</i> 3712,		99	22	Sequence 354, App	2 5	_	Sequence 11919, A	Sequence /849, Ap		671		5 6	21.0	Sequence 12914 A	D.	Seguence 20 April

ALIGNMENTS

7775, Application US/09864761

APPLICANT: Penn, Sharton G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acond.ca. X-1
CURRENT APPLICATION NUMBER: US-09/864,761
CURRENT FILING DATE: 2001-05-26
PRIOR FILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: US-60/20,456
PRIOR APPLICATION NUMBER: US-60/20,456
PRIOR APPLICATION NUMBER: US-60/20,456
PRIOR APPLICATION NUMBER: US-60/20,456
PRIOR APPLICATION NUMBER: US-60/20,366
PRIOR APPLICATION NUMBER: US-60/20,366
PRIOR APPLICATION NUMBER: US-60/236,359
PRIOR APPLICATION NUMBER: US-60/236,359
PRIOR APPLICATION NUMBER: US-60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-9
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-90
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666

APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30

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US-09-910-943-287/c

: Sequence 287, Application US/09910943

: Patent NO. US20020081610A1

: GENERAL INFORMATION:
                                   RESULT 3
US-09-860-670-161
Sequence 161, Application US/09860670; Patent No. US20020155137A1; GENERAL INFORMATION:
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SEQ ID NO 287
LENGTH: 709
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SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 7775
LENGTH: 527
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TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REFERENCE: 7529/1G148US1
CURRENT APPLICATION NUMBER: US/09/910,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: NOTHER 
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hemmati-Brivanlou, Ali APPLICANT: Altman, Curtis
APPLICANT: Ruben et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: misc_feature
LOCATION: (1)..(709)
OTHER INFORMATION: n may be a
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ORGANISM: Xenopus laevis
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19; Conserv
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EXPRESSED IN LUNG, SEPRESSED IN PLACENT
EXPRESSED IN HEART,
EXPRESSED IN BONE MARKET
EXPRESSED IN HELA, SEXPRESSED IN HELA, SEX
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IN HELA, SIGNAL = 5.2
IN ADDLT LIVER, SIGNAL = 6.4
IN FETAL LIVER, SIGNAL = 4.5
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Pred. No.
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US-09-796-692-35
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SEQ ID NO 161
                                                                                                                                                SEQ ID NO 35
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Publication No.
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Best Local
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PA127P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mannion, Jane
TITLE OF INVENTION: CONSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                 PRIOR FILING DATE:
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             FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(309)
OTHER INFORMATION: n = A,T,C or G
                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/200,779
                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/223,416
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                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-05-
                                                                                                                                                                                  OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                             NUMBER: 60/218,950
2000-07-14
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100.0%;
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Pred. No.
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Query Match Best Local Similarity

4.5%;

Score 17; Pred. No.

DB 12;

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; OTHER INFORMATION: n-A,T,C or US-09-796-692-3533
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 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3533, Application US/09796692 Publication No. US20020198362A1
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING APPLICATION NUMBER: 60/223,416
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PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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PRIOR FILING DATE: 2000-04-27
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PRIOR FILING DATE: 2000-03-17
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                                                                                          NAME/KEY: unsure
LOCATION: (296)
                                                                                                                          LOCATION: (289)
OTHER INFORMATION: n-A,T,C or
                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (277)
OTHER INFORMATION: n-A,T,C or G
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (11)
OTHER INFORMATION: n-A,T,C
                                                                                                                                                                                                                                     LOCATION: (272)
OTHER INFORMATION: n-A,T,C
                                                                                                                                                                                                                                                           NAME/KEY: unsure LOCATION: (272)
                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                               NAME/KEY: unsure
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FILING DATE: 2000-05-01
APPLICATION NUMBER: 60/202,084
FILIING DATE: 2000-05-04
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FILING DATE: 2000-05-22
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Score 17; Pred. No.
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12;
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                Length 309;
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US-10-040-739-843/c
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Best Local S
Matches 17
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SEQ ID NO 3537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3537, Application US/09878574 Patent No. US20020110548A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                           CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                          COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10040739
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VENTION: SECRETED,
EQUENCES: 1519
                                                                                                                                                                                                                                                                                                                                            Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                         Merberg,
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Lavallie, Edward
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GENERAL INFORMATION:
APPLICANT: Leach, Ma
APPLICANT: Mehraban
APPLICANT: Conley,
APPLICANT: Law, Deb
                                                                                                                      US-09-867-550-1051/c
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                                                                                                                                                                                                                                                                                                                               US-09-938-842A-1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-938-842A-1704
                                                                                    Sequence 1051, Application US/09867550 Patent No. US20020082206A1
                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1704
LENGTH: 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS,
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELLEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 843:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                          610 GAGATGCCAATCCATGG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 GAGATGCCAATCCATGG 285
                                                                                                                                                                                                                                                                             Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-JUN-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: 09/036,520
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17; Conserv
 Mehraban, Fuad,
Conley, Pamela
Law, Debbie
                                                     Leach, Martin D.
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                                                                                                                                                                                                                                                            Conservative
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100.0%; Pred. No.
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Pred. No.
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12;
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SEQ ID NO 1051
LENGTH: 1005
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Best Local Similarity
Matches 17; Conserv
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TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cell
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                  PRIOR
PRIOR
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: USSN 60/208,427 PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
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                            PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 GATGCCAATCCATGGAA 584
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                                                                                                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665
APPLICATION NUMBER: PCT/US01/00661
                                                   APPLICATION NUMBER: PCT/US01/00662
                                                                                                 APPLICATION NUMBER: PCT/US01/00663
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Pred. No
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RESULT 12
US-09-739-254-13/c
; Sequence 13, Application US/09739254
; Patent No. US20010021700A1
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; Sequence 3427, Application US/09938842A
; Patent No. US20020160378A1
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                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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SEQ ID NO 31616
LENGTH: 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3427
LENGTH: 1359
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Best Local :
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MAP TO ACO04526.1

OTHER INFORMATION: EXPRESSED IN HELDON, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.93

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.9

OTHER INFORMATION: SWISSPROT HIT: 934910, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: 934910, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: AA805896.1, EVALUE 0.00e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1041
TYPE: DNA
ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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les 17; Conserv
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nes 17; Conservative
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Pred. No.
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US-09-864-761-15087/c

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K

APPLICANT:

Sequence 15087, Application US/09864761 Patent No. US20020048763A1

RESULT 14

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; TYPE: DNA; ORGANISM: Homo sapiens US-09-904-615-13
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Matches
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SEQ ID NO 13
LENGTH: 1666
TYPE: DNA
                                                                                                                                                                                                                               SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                          Best Local Similarity Matches 17; Conserva
                                                                                                           Query Match
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CURRENT FILING DATE: 2000-12-19
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: PCT/US99/19330
EARLIER FILING DATE: 1999-08-24
EARLIER FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 60/097,917
EARLIER FILING DATE: 1998-08-25
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/904,615 CURRENT FILING DATE: 2001-07-16 PRIOR APPLICATION NUMBER: 09/511,554 PRIOR FILING DATE: 2000-02-23 PRIOR APPLICATION NUMBER: 60/097,917 PRIOR FILING DATE: 1998-08-25
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 170 SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/098,634 PRIOR FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al. TITLE OF INVENTION: 49 Human Secreted Proteins FILE REFERENCE: PZ032P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/098,634 EARLIER FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: 49 Human Secreted Proteins FILE REFERENCE: PZ032P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
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                                     271 GATGCCAATCCATGGAA 287
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740 GATGCCAATCCATGGAA 724
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100.0%; Pred. No. 12
tive 0; Mismatches
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OTHER INFORMATION: EXPRESSED IN HBL100,
OTHER INFORMATION: EXPRESSED IN PLACENTA
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OTHER INFORMATION: EXPRESSED IN LUNG, SI
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US-09-808-602-76/c
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
                                                                                                                Sequence 76, Application US/09808602
Patent No. US20020155115A1
                                                        APPLICANT: Vernet,
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Best Local (
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   APPLICANT:
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IOR APPLICATION NUMBER: PCT/USO1/00661
IOR APPLICATION NUMBER: PCT/USO1/00661
IOR APPLICATION NUMBER: PCT/USO1/00660
IOR APPLICATION NUMBER: PCT/USO1/00670
IOR APPLICATION NUMBER: US 60/234,687
IOR APPLICATION NUMBER: US 60/234,687
IOR APPLICATION NUMBER: US 9/608,408
IOR APPLICATION NUMBER: US 9/704,203
IOR APPLICATION NUMBER: US 9/774,203
IOR APPLICATION NUMBER: US 09/774,203
IOR APPLICATION NUMBER: US 09/774,203
IOR APPLICATION NUMBER: US 09/774,203
IOR FILING DATE: 2001-01-29
IMPR OF SCR IN NOW-6-6011-29
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                                                           Vernet, Corine A
Fernandes, Elma
Shimkets, Richard
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IN PLACENTA, SIGNAL = 0.95
IN FETAL LIVER, SIGNAL = 0.93
IN LUNG, SIGNAL = 2.6
IN BONE MARROW, SIGNAL = 4.9
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Search completed: January 31, 2003, Job time: 345 secs

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LENGTH: 6560
TYPE: DNA
ORGANISM: Homo sapiens
US-09-808-602-76
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Best Local
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PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding Sar
FILE REFERENCE: 15966-697 CIP
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l Similarity
17; Conserv
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                               /cgn2_6/ptodata/1/1na/5A_COMB.seq: *
/cgn2_6/ptodata/1/1na/5B_COMB.seq: *
/cgn2_6/ptodata/1/1na/6A_COMB.seq: *
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US-09-318-448-11
US-09-318-448-11
US-09-318-372-4
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US-09-318-372-4
US-09-318-372-4
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Sequence 1, Appli
Sequence 17, Appli
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Sequence 3,	Sequence 55,		, L.	, <u>.</u>	Sequence 31,	•	Sequence 23,		Sequence 25,	Sequence 25,) N	, ,		Sequence 20,		. +
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ALIGNMENTS

RESULT 1 US-09-134-001C-1264 ; Sequence 1264, Application US/09134001C ; Patent No. 6380370 ; TYPE: DNA; ORGANISM: Staphylococcus epidermidis US-09-134-001C-1264 GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCO TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NO 1264 LENGTH: 1080 Sequence 6, Application US/08480910 Patent No. 5693530 GENERAL INFORMATION: APPLICANT: Karel A. Schat, Kazuhiko Ohashi, and Priscilla APPLICANT: H. O'Connell TITLE OF INVENTION: A Marek's Disease Virus Nucleotide TITLE OF INVENTION: Sequence and Methods of Use Patent No. 5693530 NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: ADDRESSEE: Hode STREET: 1800 OF CITY: Buffalo STATE: New Yorl 309 GTAGCTATAGCAGAAGT 325 Local Similarity COUNTRY: United ZIP: 14203-2391 New York E: Hodgson, Russ, 1800 One M&T Plaza United States Conservative 4.5%; Score 17; DB 100.0%; Pred. No. 14 tive 0; Mismatches Andrews, Woods & Goodyear DB 4; Length 1080; 0 Indels 0 Gaps 0

Diskette, 3.5 inch, 1.44Mb storage

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                                                       US-09-257-580-4
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Best Local S
         Sequence 4, Application US/09257580 Patent No. 6307036 GENERAL INFORMATION:
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SEQ ID NO 1
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TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/257,580 CURRENT FILING DATE: 1999-02-25
                                                                                                                                                                                                                                                                                 LENGTH: 1146
TYPE: DNA
ORGANISM: Canis
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Tumour Suppressor Gene FILE REFERENCE: Canine p53
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U.S. SETIAL NO. 5693530 08/180,051 FILING DATE: 11 January 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect for Windows 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
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                                                                                                               1007
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                                                                                                                                           105 TGGAGCTGAAGGATGC 120
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COMPUTER: II
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SEQ ID NO 4
LENGTH: 1146
TYPE: RNA
ORGANISM: Canis
US-09-257-580-4
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CURRENT APPLICATION NUMBER: US/09/257,580
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5693530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                               TELEFAX: (716) 849-0349 INFORMATION FOR SEQ ID NO: 1:
                                                            MOLECULE TYPE: CDN
HYPOTHETICAL: yes
IMMEDIATE SOURCE:
LIBRARY: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1007 UGGAGCUGAAGGAUGC 1022
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 186
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEPRON
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS/ Microsoft Windows SOFTWARE: Wordperfect for Windows 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: U.S. Serial No. 5693530 08/180,051 FILING DATE: 11 January 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                             ORIGINAL SOURCE:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/480,910 FILING DATE: 07 June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Buffalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                               STRANDEDNESS:
               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 81.:
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RY: United States
14203-2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                              Nelson, M. Bud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08480910
                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                clone L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2: Hodgson, Russ, Andrews, Woods & Goodyear
1800 One M&T Plaza
: Marek's Disease Virus MDCC-CU41
                                                                                                                                                                              1285 nucleotides
                                                                                                                                                                                                                              (716)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karel A.
                                                                                                                                 linear
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                                                                                                                  CDNA
                                                                                                                                             single-stranded
                                                                                                                                                                                                                             849-0349
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81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Marek's Disease Virus Nucleotide Sequence and Methods of Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5 inch, 1.44Mb storage
                                                                                                                                                                                                                                                                                18617.0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16; DB Pred. No. 44;
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; LOCATION: L1 open reading frame, 725-1045
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION:
US-08-480-910-1
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Query Match
                                                                                                                                         CLONE: CLONE L1
ORIGINAL SOURCE:
ORGANTS
                                                                                                                                                                                                                                                                                                               TELEFAX: (716) 849-0349
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Control Of Marek's Disease By The
                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 08/180,051
FILING DATE: January 11, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          761 AGGAACATATGGAAAA 776
                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: CDNA
                                                                                                                                                                                                                       MOLECULE TYPE:
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ZIP: 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 4.2%;
Local Similarity 100.0%;
es 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Buffalo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                              LOCATION: L1 open reading IDENTIFICATION METHOD: by OTHER INFORMATION:
                                                                                                             CELL TYPE:
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                                                                                                                                                                                                                                                                                                     ENGTH:
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14203-2391
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                                                                                                                                                                                                                                                                                      nucleic
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                                                                                                          narek's Disease Virus
MDCC-CU41
E: virus
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                                                                                                                                                                                                                                                                                                   1285 nucleotides
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                                                                                                                                                                                                                                                      linear
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   4.2%;
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Pred. No.
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    Score 16;
                                                             frame, 725-1045 experiment
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    DB 5;
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   Length 1285;
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; LOCATION: (1302)
US-09-500-569-17
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US-09-500-569-17/c
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                        NUMBER OF SEQ :
SOFTWARE: Micro
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 17
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                                                                                                                                                                                                                    Sequence 9, Application US/09461474 Patent No. 6278042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Plant Caffeic acid 3-0-Methyltransferase Homologs FILE REFERENCE: BB1327 US NA CURRENT APPLICATION NUMBER: US/09/500,569 CURRENT FILING DATE: 2000-02-09 EARLIER APPLICATION NUMBER: 60/119,587
                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1314
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
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APPLICANT: Shen, Jennie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cahoon, Rebecca E.
                                                                                                APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
                                                                    EARLIER APPLICATION NUMBER: 60/112,562 EARLIER FILING DATE: 1998-12-16
                                                                                                                                                                                         APPLICANT: Allen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure LOCATION: (472)
TYPE: DNA
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                                                                                                                                                                                                                                                                                                           1247 CCCAAGCCGGAGTCTC 1232
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(1156)
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(1262)
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(1180)
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                                             Office 97
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US-09-221-017B-811/c
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US-09-461-474-9
                         ; NAME/KEY: misc_feature ; LOCATION: 1...4413 US-09-221-0178-811
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Best Local Similarity
Matches 16; Conserv
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                 TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4413 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSON DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FTI.ING DATE: 30-JAN 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                        FEATURE:
                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-APR-:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                             HYPOTHETICAL:
                                                                                                                                          MOLECULE TYPE:
                                                                                                                 NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 755 PAGE CITY: Palo Alto
                                                                                                                                                                                                                                                                                                    NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PP2911 FILING DATE: 09-APR-1998
                                                                                     ORGANISM:
                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                    nucleic acid
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                                                                                                                 UWKNOWN
                                                                                     PORYPHYROMONAS GINGIVALIS
                                                                                                                                                         circular
                                                                                                                                          DNA (genomic)
                                                                                                                                                                        double
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Pred. No.
                                                                                                                                                                                                                                                                                                      27340-20021.00
Score 16;
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Length 4413;
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US-09-318-448-11
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US-08-735-609-4/c
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Patent No. 6210950
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CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Johnson, William G.
APPLICANT: Stentoos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
   INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18596
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10134 GATGGTGATGGAGATG 10149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAS: (415) 397-8338
FORMATION FOR SEQ ID NO: 4:
                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,
                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 GATGGTGATGGAGATG 274
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Local Similarity 100.0%; Pred. No.
les 16; Conservative 0; Mismatr)
                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Medlen & Carroll, LI
STREET: 220 Montgomery Street,
CITY: San Francisco
STATE: California
                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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Amalfitano, Andrea
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                                                                                                                                                                                                                               IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                                          40,027
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                                                                      UM-02484
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US-08-735-609-4/c
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                                                              Matches
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Patent No. 5994132
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey
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Matches 16; Conserv
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Best Local :
27052 CAACATGCTTTGACTG 27037
                                                                                                                                                                                                     TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27052 CAACATGCTTTGACTG 27037
                               212 CAACATGCTTTGACTG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                             Local
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TOPOLOGY: 11r
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                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-OCT-1996
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Ingolla, Diane E.
                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumar-Singh, Rajendra
Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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llarity 100.0%; Pred. No.
Conservative 0; Min-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States Of America
                                                        4.2%; 50
100.0%; Pr
                                                                           Score 16;
Pred. No.
                                                              Mismatches
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                                                                           DB 2;
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37;
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                                                                                          Length 34303;
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RESULT 14
US-09-244-752-4/c
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US-09-315-372-4/c
                                                                                                                                                                                   Sequence 4, Applic Patent No. 6063622
                                                                                                                    GENERAL INFORMATION:
APPLICANT: Chamber:
APPLICANT: Amalfit:
APPLICANT: Hauser,
                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local :
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Patent No. 6
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LENGTH: 34303 harman
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                                                                                                                                                                                                                                                                                          27052 CAACATGCTTTGACTG 27037
                                 CORRESPONDENCE ADDRESS:
                                                               APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/315,372
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APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn polonomia
 STREET:
                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                           Local
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STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States Of America ZIP: 94104
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16; Conserv
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                                                                                                                                                                                                       Application US/09244752
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2: Medlen & Carroll, LLP
220 Montgomery Street, Suite 2200
                                                                                               Amalfitano, Andrea
Hauser, Michael A.
Kumar-Singh, Rajendra
                                                                                                                                                    Chamberlain, Jeffrey
                                                                                                                                Amalfitano,
                                                                                                                                                                                                                                                                                                                                                           Conservative
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/desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                                                                                                                         4.2%; Score 16;
100.0%; Pred. No.
tive 0; Mismatc
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37;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

STATE: California

United States Of America

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US-09-245-497-4/c
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NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REGISTRATION NUMBER: UM-0:
TELEPHONE: (415) 397-8338
INFORMATION: FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Chamber
APPLICANT: Amalfit
APPLICANT: Hauser,
APPLICANT: Kumar-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09245497 Patent No. 6083750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.2%; Score 16; Best Local Similarity 100.0%; Pred. No Matches 16; Conservative 0; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27052 CAACATGCTTTGACTG 27037
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/245,497
FILING DATE:
                                                                                                                                                                                                                                                                                                                            APPLICANT: Hauser, Michael APPLICANT: Kumar-Singh, Rajendra APPLICANT: Kumar-Singh, Rajendra APPLICANT: Hartigan-O'Connor, Dennis J. TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: Medlen & Carroll, LLP ADDRESSEE: Medlen & Carroll, LLP
                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
APPLICATION NUMBER: (
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TOPOLOGY: linear
MOLECULE TYPE: othe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/244,752
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 CAACATGCTTTGACTG 227
                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chamberlain, Jeffrey S.
Amalfitano, Andrea
                                                                                                                                                                                                                                                                                 United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
          08/735,609
<B) FILING DATE:
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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-09-245-497-4
Search completed: January 31, 2003, 03:51:24
Job time: 133 secs
                                                                  8
                                                                                              δÃ
                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                              27052 CAACATGCTTTGACTG 27037
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                         NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
                                                                                              212 CAACATGCTTTGACTG 227
                                                                                                                                                                                                                                                              STRANDEDNESS:
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                             Score
       34590
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Match
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13.0
13.0
11.9
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7.9
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Gapop 60.0 , Gapext 60.0
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378
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gb_htc:*
gb_est3:*
gb_est4:*
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      451
386
439
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17
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BG197212
AQ035618
AQ035738
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BM987874 UI-H-CO0-
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AI459918 ar80h09.x
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BQ579887 BG409744 BM635028

ALIGNMENTS

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BM6537418 170006875

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AV605455 AV605117 BF713089 AW464207 AZ364217 BQ600629 BQ599839 BQ597758

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FEATURES Source		JOURNAL COMMENT	TITLE	REFERENCE	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 1 BM987874/c LOCUS DEFINITION
Location/Qualifiers 1451	Tissue Procurement: Dr. Jose Mercuende CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Seq primer: M13 FORWARD	Unpublished (1997) Contact: Robert Strausberg, Ph.D.	NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Eukaryota; Metazoak Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 451)	human. Homo sapiens	BM987874.1 GI:19707263 EST.	BM987874 UT-H-COO-asz-a-11-0-UI.sl NCI_CGAP_Sub9 Homo sapiens cDNA clone

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RESULT 2
AA743908/c
                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
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                                                                                                  source
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                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Unsert Length: 508 Std Error: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 386)
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                                                                                                                ert Length: 508 Std Error: 0.00 primer: -40ml3 fwd. Er from Amersham h quality sequence stop: 234.
Location/Qualifiers
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/lab_host="bHIDB (Life Technologies)"
/note="vector: p773-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa with
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
carcinoma, Bladder carcinoma, Brain oligodenroga;
NCI_CGAP_Sub9 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are CGTC, AACG, GGGCC,
GGAAG, TAACC, ATGC, ARGA, ATCAC. For additional
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1322779"
/clone_lib="NCI_CGAP_Kid3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_SEQ-ATGG"
93 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      information, contact: Bento Soares, bento-soares@uiowa.edu
TAG_LIB=UI-H-CO0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Sub9"
/tissue_type="mixed"
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100.0%; Pr
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Pred. No.
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o sapiens cDNA
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 451;
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VERSION

FEATURES

Query Match

13.0%;

Score 49;

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Length 439;

COMMENT

TITLE

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REFERENCE
AUTHORS
      BASE COUNT
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ORGANISM
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VERSION
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AI459918/c
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ORIGIN
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI459918 439 bp mRN ar81h09.x1 Barstead colon HPLRB7 Homo
                                                                                                                                                                                                                                                                                               High quality sequence stop:
                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.linl.gov) for
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMAGE: 2151713 3', mRNA sequence.
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    115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
    a
                                      /note-Torgan: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
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77 c 73 g
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b; Pred. No. 2.9
0; Mismatches
                        pT7T3 vector. Library constructed by Bob
81 g
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                                                                                                                                                                                                                                        Contact: Scott J. Cain
Athersys, Inc.
3201 Carneyie Ave, Cleveland, OH 4
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 417.
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 349)
                                                                                     SSD
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CIT-HSP-2319N3.TF
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1 (bases 1 to 806)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Coln, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Kilka, A., Hess, J., Cothren, K., Lo, K., Offenbacher (J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                 AQ035618.1
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                                                                                                                                 sequence.
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RST16451 Athersys RAGE Library Homo sapiens
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a 187 c 155 g 205 t 7 others
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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/cell_line="HT1080"
/coll_specification of Genome-wide Protein Expression
                                                                                                 GI:3301715
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Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                        Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                      Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Other GSSs: CIT-HSP-2321C21.TR
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CIT-HSP-2321C21.TF CIT-HSP Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
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Other_GSSs: CIT-HSP-2319N3.TR
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/db_xref="taxon:9606"
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Blotechnol. 19 (5), 440-445 (2001)
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RST30277 Athersys RAGE Library |
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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Bex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2321C21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib-"CIT-HSP"
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                                                                                                     5.6%;
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                                                                                                  Score 21; DB 12; Length 357; Pred. No. 1.7;
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1.3e-05;
hes 0;
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ACCESSION
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                                                                               RESULT 9
BG223756
LOCUS
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                                                           DEFINITION
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BQ597872/c
LOCUS
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Query Match
Best Local :
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BG223756
BG223756.1 GI:12709277
EST.
                                                                    1M00018F10a Bovine Mixed
                                                                                              BG223756
                                                                                                                                                                                                                                                     h 5.6%; So Similarity 100.0%; 1 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. Chris Tuggle, Iowa State University cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA sequence: 1-22, >AT_rich#Low_complexity

Seq primer: M13 FORWARD
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201 Kildee Hall, Ames, IA 50011-3150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular Genetics Laboratory, Department
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Sus scrofa
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MI-P-A2-afh-a-04-1-UM.sl, mRNA sequence
BQ597872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 5152942401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Tuggle CK
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The M1-Pac library is derived from anterior pituitary at estrus contact in the structure of the library from withis clone was derived, please visit our web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-A2-sth-a-04-1-UM"
/clone_lib="MI-P-A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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0; Mismatches
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1.7;
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BASE COUNT
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AV605455.1
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                                                                                       Takasuga, A.,
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                            Bos taurus
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Bos taurus
                   bovine ESTs
                                    poly(A) tall-removed
                                                                        and Sugimoto,Y.
                                                                                                                           Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence best matches gb:AF026293 (Homo sapiens chaperonin containing t-complex polypeptide 1, beta subunit (Cctb) mRNA, complete cds. 12/1998) in GenBank main database at E-value of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. 1 (bases 1 to 526) Moore, S.S., Hansen, C., Li,C., Fu,A., Meng,Y., Li,G., Mur Dixon, M. and Christopherson, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA's from bovine mixed skeletal muscle Unpublished (2001) Contact: Dr. Stephen S. Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smoore@afns.ualberta.ca
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Dept of AFNS, University of Alberta
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780 492 4265
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                           lishment of a high throughput EST sequencing system using a) tail-removed cDNA libraries and determination of 36,000
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Acids Res. 29 (22),
                                                                                                                                                                                                                                                                  sequence.
                                                                                                                                                                                                                                                                                Bos taurus kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="muscle"
/dev_stage="Young adult"
/lab_host="xL1-BlueMRF-strain"
/lab_host="xL1-BlueMRF-strain"
/note="Organ: Skeletal muscle; Vector: Uni-2ZAPXR;
ECOR I; Site_2: xho I"
99 c 119 g 153 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Bovine Mixed Skeletal Muscle cDNA Library"
/sex="two males and one female mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                 Hirotsune, S., Itoh, R., Jitohzono, A.,
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                                                                                 Suzuki, H., Aso, H.
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cora; Bovoidea;
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                                                                                                                                      Bovoidea;
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AV605117
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AV605117
                                                                                                                                                                                                                Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                   Single pass sequencing.
                                                                                                                                                                                               Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                 Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                             poly(A) tail-removed
bovine ESTS
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                                                                                                                                                                                                                                                                                                                                                                                                and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                          Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV605117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing.
This clone was obtained from a polyA-deleted Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae;
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Shirakawa Institute of Animal Genetics
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Contact: Yoshikazu Sugimoto
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                                                                                                                                                               clone was obtained from a polyA-deleted
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                                                                                                                                                                                                                                                                                                                                                       lishment of a high throughput EST sequencing system using a) tail-removed cDNA libraries and determination of 36,000
                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="EIKIO26H04"
/clone="Ib="Bos taurus k
/tissue_type="Kidney"
/dev_stage="fetus"
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136 c 110 g 153 t 3 others
                  'lab_host="DH10B"
                                                                                                                                                 Location/Qualifiers
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/tissue_type="kidney"
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="E1KI028H04"
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 pZL1; Site_1:
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21;
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Sall; Site_2: Not1; Poly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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BF713089/c
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     Query Match 5.6%; Score 21; DB 12; Length 547; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 21; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence contained an oilgo-dT track that was present in the oilgonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oilgo-dT track served to verify it as a clone from the non-normalized hypothalamus at estrus day 12 library cDNA Library Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be available through Research Genetics (www.resgen.com) seq primer: M13 Forward polytheres.
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Town State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF713089 547 bp mRNA linear ES'MI-P-H3-adm-h-03-1-UM.sl MI-P-H3 Sus scrofa cDNA clone MI-P-H3-adm-h-03-1-UM 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                      Seq prime.
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BF713089.1 GI:12012570
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mmalia; Euthoria; Cetartiodactyla; Suina; Suidae; Sus.
(bases 1 to 547)
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                                                                                                                                                                                /lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoR; The MI-PH3 library is derived from hypothalamus at estrus day 12. For a detailed description of the library from which this clone was derived, please visit our web site at http://nigat.geography.
                                                                                                   TAG_TISSUE-hypothalamus at estrus day 12
TAG_SEQ-GGTTAA"
107 c 102 g 181 t
                                                                                                                                                      http://pigest.genome.lastate.edu/
TAG_LIB-MI-P-H3
                                                                                                                                                                                                                                                                                       /strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-H3-adm-h-03-1-UM"
/clone_11b="MI-P-H3"
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       0;
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AZ364217
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350 GAAGGAAGGTACCATTGGAGA 370
                                                                                       Local Similarity 100.
nes 21; Conservative
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Fax: 217 244 5617
Email: h-lewin@uluc.edu
Email: h-lewin@uluc.edu
Email: h-lewin@uluc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi 9:
Cross_match from Washington University Genome Center PHRAP suite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: AGCGGATAACAATTTCACACAGGA
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Plate: BP230015A10 row:
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Sequences submitted are vector free and at least 200 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cow.
Bos taurus
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AW464207
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 569.
Location/Qualifiers
                                                                                                                                                                                          /note-"Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. *

a 112 c 144 g 150 t 3 others
                                                                                                                                                                                                                                                                                                                                            /sex="female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP230015A10F9"
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                                                                                                                                                             219 CTTTGACTGTTGAAAAGAGAC 239
       BQ600629
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Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: P column: 18
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                            Similarity 100
21; Conservative
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Location/Qualifiers
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Roye, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IM0110P18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone uugc1m0110p18 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 589)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampletillin resistance."
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/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C5/BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg.,
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/clone="UUGC1M0110P18"
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Search completed: January 31, 2003, 05:14:00 Job time: 2258 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
434 GAAGGAAGGTACCATTGGAGA 414
                                          350 GAAGGAAGGTACCATTGGAGA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cktuggle@lastate.edu
Tissue Procurement: Dr. Chris Tuggle, Iowa State University
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
The following repetitive elements were found in this cDNA
sequence: 1-22, >AT_rich#Low_complexity
POLYA-Yes
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Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 611)
                                                                                                        Similarity
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                                                                                      Conservative
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                                                                                                                                                                                                                                                   /Clone_lib=MI-P-E7"
//lab_host="DH10B (Life Technologies)"
//lab_host="DH10B (Life Technologies)"
//note="Vector: pSPORT1; Site_1: Not I; Site_2: EcoRI; The MI-P-E7 library is derived from the following tissue(e): preelongation day 12 conceptus. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.lastate.edu/.
TAG_LIB-MI-P-E7
                                                                                                                                                                                                             TAG_TISSUE-preelongation_d_12_conceptus
TAG_SEQ-GTGAGA"
                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-E7-agz-d-10-1-UM"
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Copyright (c) 1993 - 2003 Compugen Ltd
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AAS37164 standard; cDNA; 378

ВP

17-DEC-2001 AAS37164;

(first entry)

Williams LT, Escobedo J, Innis MA, G. Reinhard C, Randazzo F, Kennedy GC, Drmanac R, Crkvenjakov R, Dickson M, Leshkowitz D, Kita D, Garcia V, Jone WPI; 2001-530177/58 (CHIR) CHIRON CORP. (HYSE-) HYSEQ INC. 09-MAR-2000; 2000US-0188609 09-MAR-2001; 2001WO-US07787 13-SEP-2001, WO200166753-A2 Human; cancer; breast; Novel human diagnostic and therapeutic gene #222. Homo sapiens lung; colon; prostate; cytostatic; diagnostic; ss Jones WL, Garcia PD, Sudduth-Klinger J;
Pot D, Kassam A, Lamson G;
I, Drmanac S, Labat I;
nes WL, Stache-Crain B;

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ARSULT 2
AAS37237
ID AAS3
XX AAS3
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Best Local
                      09-MAR-2000; 2000US-0188609
                                             09-MAR-2001;
(CHIR ) CHIRON CORP
                                                                                             WO200166753-A2
                                                                                                                    Homo sapiens
                                                                                                                                                         Novel human diagnostic and therapeutic gene #295
                                                                                                                                                                                                                                AAS37237 standard; cDNA;
                                                                                                                                        Human; cancer;
                                                                                                                                                                                      17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to new polynucleotides and polypeptides, useful fo diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS3938 represent novel human diagnostic and therapeutic coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 378 BP; 100 A; 76 C;
                                                                                                                                                                                                                                                                                           361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378;
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                                             2001WO-US07787
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                    (first entry)
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                                                                                                                                        breast;
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                                                                                                                                       lung;
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                                                                                                                                      colon;
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Pred. No. 1.6e-187;
Mismatches 0;
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                                                                                                                                    prostate; cytostatic;
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                                                                                                                                 diagnostic;
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AAS37218
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Best Local Similarity
Matches 238; Conserv
                                          (CHIR )
(HYSE-)
                                                                                                                    09-MAR-2000;
                                                                                                                                                              09-MAR-2001; 2001WO-US07787
                                                                                                                                                                                                                  13-SEP-2001
                                                                                                                                                                                                                                                            WO200166753-A2.
                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic and therapeutic gene #276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to new polynucleotides and polypeptides, useful fo diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with differentially expressed genes correlated with differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39338 represent novel human diagnostic and therapeutic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS37218 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 670; 1193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239
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Reinhard C, Randazzo F, Kennedy GC, Pc
Drmanac R, Crkvenjakov R, Dickson M, I
Leshkowitz D, Kita D, Garcia V, Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
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                                                                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGA 238
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                                                                                                                                                                                                                                                                                                                                                        cancer;
                                       CHIRON CORP
HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 BP; 90 A; 64 C; 78 G; 89 T; 1 other;
                                                                                                               2000US-0188609
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lung and colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327
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Pred. No. 2.6e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                            prostate; cytostatic;
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C, Pot D, Kassam A, L
C, Camanac S, Labat I
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es WL, Stache-Crain
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                                                                                                                                                                                                                                                                                                                                       diagnostic;
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Williams LT,

Escobedo

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Innis

MΑ,

Garcia

PD,

Sudduth-Klinger

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Best Local Similarity
             Williams LT,
Reinhard C,
Drmanac R, C
                                                 (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                              09-MAR-2000; 2000US-0188609
                                                                                                09-MAR-2001; 2001WO-US07787
                                                                                                                                      WO200166753-A2
                                                                                                                                                                    Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic;
                                                                                                                                                                                        Novel human diagnostic and therapeutic gene #300.
                                                                                                                                                                                                                                                   AAS37242 standard; cDNA; 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a differentially expressed genes correlated with a differentially expressed gene product in a test sample derived from a tenuour growth by modulating expression of a gene product. AAS36343-AAS39338 represent novel human diagnostic and therapeutic coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences of the invention.
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                                                                                                                                                                                                                                                                                                       232
                                                                                                                                                                                                                                                                                                                                            172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac R, Crkvenja
Leshkowitz D, Kita
                                                                                                                                                                                                                                                                                                                         239
                                                                                                                                                                                                                                                                                                                                                             179
                                                                                                                                                                                                                                                                                                                                                                                112
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                                                                                                                                                                                                                                                                                                                                                                                                                      52
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                                                                                                                                                                                                                                                                                             polynucleotides and polypeptides, useful atment of breast, lung and colon cancer -
                                                                                                                                                                                                                                                                                                                                              ACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTTGAAAAAGAGA 238
                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAAACACCCAAGCCGGAGTCTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGAT 118
                                                                                                                                                                                                                                                                                                                                    GGAAAACACCCAAGCCGGAGTCTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                          238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 665; 1193pp; English.
, Escobedo J, Innis MA,
Randazzo F, Kennedy GC,
Crkvenjakov R, Dickson M,
D, Kita D, Garcia V, Jor
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                              (first entry)
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Crkvenjakov i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 64 C; 81 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
  Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones
    Garcia PD, Suduut....
Pot D, Kassam A, Lar
Pot D, Kassam I,
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Drmanac S, Labat :
s WL, Stache-Crain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.6e-114;
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S, Labat I;
                           Sudduth-Klinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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ABA20368
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                          04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                            immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulne antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; antiparasitic; cardiant; immune disorder; cardiovascular disorder; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                    31-JAN-2000;
                                                                                             17-JAN-2001;
                                                                                                                          16-AUG-2001
                                                                                                                                                   WO200159063-A2
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                          neurological disease;
                                                                                                                                                                                                                                                                        Human; nootropic; neuroprotective; cytostatic;
immunosuppressive; antiinflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                Human nervous system related polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                  23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                              ABA20368;
                                                                                                                                                                                                                                                                                                                                                                                                      ABA20368 standard; DNA; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39318 represent novel human diagnostic and therapeutic coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 318 BP; 90 A; 63 C; 76 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides, useful treatment of breast, lung and colon cancer .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTTAATGTTCTTTGGAATAAAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAACACCCAAGCCGGAGTCTCTCACAAGCTTGAATGTGTGTTTCTGGAGCTGAAGGAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCTCCCTGCCAAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 671; 1193pp; English.
        ; 2000US-0179065.
; 2000US-0180628.
; 2000US-0184664.
; 2000US-0186350.
; 2000US-0189874.
                                                                                              2001WO-US01334
                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.4%;
                                                                                                                                                                                                       infection;
                                                                                                                                                                                                                                            ng; antianaemic; antiarthritic; cancer; cerebroprotective; antinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 232;
Pred. No.
                                                                                                                                                                                                    nephrotropic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
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                                                                                                                                                                                                                                                                     antibacterial; vulnerary;
                                                                                                                                                                                                                                                                                   dermatological;
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                                                                                                                                                                                                                                                                                                                  NO 12699
                                                                                                                                                                                                 vaccine;
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18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000; 11-JUL-2000;

2000US-0198123 2000US-0205515

2000US-0209467.
2000US-0214886.
2000US-02154886.
2000US-0216687.
2000US-0216880.
2000US-0217496.
2000US-0217496.
2000US-0220964.
2000US-0220964.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225266.
2000US-0225268.
2000US-0225279.
2000US-0225279.
2000US-0225279.
2000US-0225279.
2000US-0225279.
2000US-0225279.
2000US-0225279.

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are
                                                                                                                                                                                                                                  17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                           Nucleic acids encoding useful for preventing, cancers and metastases
                                                                                                                                                                                                                                                                                                                                                                                                                              20 - OCT - 2000;

08 - NOV - 2000;

09 - NOV - 2000;

01 - NOV - 2000;

01 - NOV - 2000;

02 - NOV - 2000;

03 - NOV - 2000;

04 - NOV - 2000;

05 - NOV - 2000;

06 - NOV - 2000;

07 - NOV - 2000;

17 - NOV - 2000;
                                                                  Disclosure;
                                                                                                                                                                               Rosen
                                                                                                                                                                                                         ( HUMA - )
                                                                                                                                                  2001-541565/60.
                                                                                                                                                                               CA,
                                                                                                                                                                                                         HUMAN
                                                                                                                                                                            Barash SC,
                                                                  SEQ ID
                                                                                                                                                                                                                               2000US-0241809
2000US-0241809
2000US-0241809
2000US-02446474
2000US-0246477
2000US-0246477
2000US-0246477
2000US-0246523
2000US-0246523
2000US-0246523
2000US-0246523
2000US-0246523
2000US-0246523
2000US-0246523
2000US-0246523
2000US-0246511
2000US-0246511
2000US-0249207
2000US-0249207
2000US-0249211
2000US-0249216
2000US-0249216
2000US-0249216
2000US-0249216
2000US-0251160
2000US-0251160
2000US-02511888
2000US-0251889
2000US-0251999
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2000US-0241785
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                                                                                                                                                                                                         SCI
                                                       12699; 1701pp + Sequence Listing; English.
                                                                                              3224 human
diagnosing
                                                                                                                                                                            Ruben
                                                                                                                                                                            MS
                                                                                               nervous system antigen polypeptides, and/or treating nervous system
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14 - AUG - 2000 22 - AUG - 2000 22 - AUG - 2000 23 - AUG - 2000 21 - SEP - 2000 21 - SEP - 2000 22 - AUG - 2000 23 - AUG - 2000 24 - SEP - 2000 25 - SEP - 2000 26 - SEP - 2000 27 - SEP - 2000 28 - SEP - 2000 29 - SEP - 2000 21 - SEP - 2000 22 - SEP - 2000 23 - SEP - 2000 24 - SEP - 2000 25 - SEP - 2000 27 - SEP - 2000 29 - SEP - 2000 20 - SEP - 2000 21 - SEP - 2000 22 - SEP - 2000 23 - SEP - 2000 24 - SEP - 2000 25 - SEP - 2000 27 - SEP - 2000 29 - SEP - 2000 21 - SEP - 2000 21 - SEP - 2000 22 - SEP - 2000 23 - SEP - 2000 24 - SEP - 2000 25 - SEP - 2000 27 - SEP - 2000 29 - SEP - 2000 20 - CCT - 2000 21 - CCT - 2000 22 - CCT - 2000 23 - CCT - 2000 24 - CCT - 2000 25 - CCT - 2000 27 - CCT - 2000 28 - CCT - 2000 29 - CCT - 2000 21 - CCT - 2000

2000US-0226681
2000US-0226681
2000US-0227009
2000US-0229343
2000US-0229343
2000US-0229343
2000US-0229343
2000US-0229343
2000US-0231244
2000US-0231244
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2000US-0231244
2000US-0231268
2000US-0231268
2000US-0232080
2000US-0232080
2000US-0232399
2000US-0233993
2000US-0233993
2000US-0234274
2000US-0233964
2000US-0234274
2000US-0234284
2000US-0234384

SSSS

printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match Best Local :

Similarity

5.0%;

Score 19; Pred. No. 110 G;

9; BB

22;

Length

Sequence

527 BP;

175

A;

99

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143 T; 0 other;

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RESULT 6
ABA61650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
xx
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                 Claim 1; SEQ ID NO
                                                                                                                                                       Human genome-derived single exon nucleic
                                                                                                                                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
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                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human foetal liver single exon nucleic acid probe #9955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA61650 standard; DNA; 527 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA61650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                    SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCTGGAGCTGAAGGATG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCTGGAGCTGAAGGATG 285
 The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
19; Conserv
                                                                                                                                            gene expression
                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                        ; 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-023669.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 105 A;
                                                                                                           9955; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.0%;
                                                                                                                                                                                                                  Chen W,
for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 C; 82 G;
                                                                                                                                           le exon nucleic acid probes useful in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No.
                                                                                                                                                                                                                  Rank
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RESULT 7

ABA29309
AD ABA29309
AD ABA29309
AC ABA2
XX
AC ABA2
XX
AC ABA2
XX
BA ABA2
AC ABA2
AC
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                                                                                                         measuring human gene expression in a sample derived from human heart. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systelegical congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                       specification,
                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                            Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn
                                                                                                  Note:
                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                      hearts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        congenital heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene expression; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe #7775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 TGTTCTTTGGAATAAAAAC 180
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                                         ftp.wipo.int/pub/published_pct_sequences.
                                                             The sequence data for this patent did not fication, but was obtained in electronic for
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                ID No 7775; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US00666
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                                                                                                                                                                                                                                                                                                                                                                                                                       acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heart; microarray; vas
hypertension; cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                  probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vascular system; probe;
                                                               ot form
format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arrhythmia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                             directly
                                                                                                                                  vascular system
hmias and
                                                                                                                                                                                                                                                                                                    probes for
                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                             om WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Query Match Matches

Local

l Similarity 19; Conserv

Conservative

5.0%; 5c. 100.0%; Pr

Score 19; DB; Pred. No. 9; 0; Mismatches

9; 8G

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Indels

0

Gaps

0

22; 0 other;

Length 527;

Sequence 527

BP; 175

A; 99 C; 110 G; 143 T;

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RESULT 9
AAK35845
ID AAK3
XX
AC AAK3
XX
DT 06-N
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                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
AAK09951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             дb
                                                                                                   Matches
                                                                                                         Query Match
Best Local :
      06-NOV-2001
                     AAK35845;
                                                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                   AAK35845
                                                                                                                                                                                                                   Single
brains
                                                                                                                                                                                                                                        WPI;
                                                                                                                              Sequence 527
                                                                                                                                                   epilepsy and cancers.
                                                                                                                                                                                                Example 4; SEQ ID NO: 9942; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                  27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                      Penn
                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                        477
                                                                                   162 TGTTCTTTGGAATAAAAAC 180
                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                                       03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                         30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                      WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                  epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed emicroarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK09951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK09951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                                                                                                -SEP-2000;
                                                                      TGTTCTTTGGAATAAAAAC 495
                                                                                                                                                                                                                                                      SG,
                                                                                                                                                                                                                                       2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTCTTTGGAATAAAAC
                                                                                                  l Similarity
19; Conserv
                                                                                                                                                                                                                      exon nucleic acid probes for analyzing
                                  standard;
                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
2000US-0236359
                                                                                                  Conservative
    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             expressed single
                                                                                                                               BP; 175
                                                                                                                                                                                                                                                                                                                    2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                         2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                   88.
                                                                                              5.0%; 5.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                             A; 99 C;
                                                                                                                                                 The present sequence
                                                                                                                                                                                                                                                     Chen
                                                                                                                                                                                                                                                                                                                                                                                                                exon;
                                  527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527
                                                                                                                                                                                                                                                                                                                                                                                                        disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                     ξ
                                                                                                        Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                            110 G; 143 T;
                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                     Rank
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      expression analysis; probe;
multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                            probe
                                                                                                                                                                                                                                                     DR;
                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                               22;
                                                                                                                                                 19
                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                             IJ
                                                                                                0;
                                                                                                                            other;
                                                                                                                                                 one of
                                                                                                                                                                                                                       gene expression
                                                                                                              Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                             SO:
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             9942
                                                                                                                                               the probes
                                                                                                0,
                                                                                                                                                                                                                       'n
                                                                                               Gaps
                                                                                                                                                of the
                                                                                                                                                                                                                       human
                                                                                              0
RESULT 10
AAI17155
ID AAI17
XX
AC AAI1
XX
DT 12-(
XX
DE Prc
XX
KW Pr
KW C6
XX
CS H
XX
PN (
XX
PD
XX
PD
XX
PR
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Matches
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04-FEB-2000; 2000US-0180312
                                                                                                                                                                                    Probe #7088 for gene expression analysis in human cervical cell sample.
                           30-JAN-2001; 2001WO-US00670.
                                                          09-AUG-2001
                                                                                         WO200157278-A2
                                                                                                                      Homo sapiens
                                                                                                                                                   cervical
                                                                                                                                                                                                                                                        AAI17155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic ac probes which are derived from genomic sequences expressed in the bone marrow. They can be used to measure gene expression in bone samples, which may enable the improved diagnosis and treatment of such as lymphoma, leukaemia and myeloma. The present sequence is the probes of the invention.
                                                                                                                                                                                                                          12-OCT-2001
                                                                                                                                                                                                                                                                                  AAI17155 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                            477
                                                                                                                                                                                                                                                                                                                                                                       162 TGTTCTTTGGAATAAAAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                         TGTTCTTTGGAATAAAAAC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG,
                                                                                                                                                                 human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bone marrow expressed single exon
                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULAR DYNAMICS INC
                                                                                                                                                  uman; microarray; gene expression; cervical epithelial cell;
cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 A; 99 C;
                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed exon; gene expression ar
; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                5.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                  527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon nucleic acid probes useful for n human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe
                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               marrow
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RESULT 11
AAI41562
ID AAI41
XX AAI41
XC AAI41
XX Probe
XX Probe
XX Probe
XX Probe
XX Probe
XX Probe
XX Pono
XX Homo
XX WO20(
XX W020(
XX W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                           04-FEB-2000; 2
26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                           W0200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #10248 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI41562 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 TGTTCTTTGGAATAAAAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocal.
                        SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTCTTTGGAATAAAAAC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; SEQ ID No 7088; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Similarity
19; Conserv
                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527
                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                             ; 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-06323687.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.0%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0224263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 175 A; 99 C; 110 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527
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Pred. No
                      Rank DR;
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Mismatches
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Matches 19
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
27 - SEP - 2000;
                                                                                                                                                                                                                                                                                                                                                             Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary hemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary cillary dyskinesis; pulmonary hypertension;
                                                                                                                                                                   04-OCT-2000;
                                                                                                                                           (MOLE-)
                                                                                                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon probe from lung
                                                                                                                                                                                                                                                                                    15-NOV-2001.
                                                                                                                                                                                                                                                                                                           WO200186003-A2
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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19; Conserv
                                                                                                                                         MOLECULAR DYNAMICS INC
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2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
2000US-236359P.
2000US-2024263.
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                                                                                                                                                                                                                                                           2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID No 10248; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                          disease
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                                                                                                                  Chen W,
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The invention relates to nucleic acid probes for m

measuring

spatially-addressable : asuring gene expression

set of on in a s

single

derived exon Claim 1;

SEQ ID No 10069; 634pp; English.

Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples -

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RESULT 13
ABA17906
ID ABA17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 19
                                                                                                                                                                                                   Human; nootropic; neuroprotective; cytostatic; dermatological; virusimunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulne antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiuleer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung and the contacting the array with the collection of detectably labeled nucleic acids derived from human lung and the collection of detectably labeled nucleic acids derived from human lung and the collection of detectably labeled nucleic acids derived from human lung and the collection of detectably labeled nucleic acids derived from human lung and the collection of detectably labeled nucleic acids derived from human lung and the collection of detectably labeled nucleic acids derived from human lung and the collection of detectably labeled nucleic acids derived from human lung and the collection of detectably labeled nucleic acids derived from human lung and the collection of detectably labeled nucleic acids derived from human lung and the collection of detectably labeled nucleic acids derived from human lung and the collection detectably labeled nucleic acids derived from human lung and the collection detectably labeled nucleic acids derived from human lung and the collection detectably labeled nucleic acids derived from human lung and the collection detectably labeled nucleic acids derived from human lung and the collection detectably labeled nucleic acids derived from human lung and the collection detectably labeled nucleic acids derived from human lung and the collection detectably labeled nucleic acids derived from human lung and the collection detectably labeled nucleic acids derived from human lung and the collection detectably labeled nucleic aci
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                                                                                                                             Homo sapiens
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                                                                                                                                                                                    neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 TGTTCTTTGGAATAAAAC 180
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The sequence data for this patent did

The sequence data for this patent did
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19; Conserv
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                                                                                                                                                                                    disease;
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                                                                                                                                                                                    infection;
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2000US-0198123.
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                                                      Rosen CA,
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2000US-0246476.
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31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 17-MAR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000; 11-JUL-2000;

2000US-0179065.
2000US-01846648.
2000US-01846350.
2000US-0189874.
2000US-0198123.
2000US-029467.
2000US-0214886.
2000US-0215135.
2000US-0216847.
2000US-0216847.
2000US-0217487.
2000US-0217487.
2000US-0217487.

17-JAN-2001; 2001WO-US01354

WO200157182-A2

Homo sapiens.

09-AUG-2001.

Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.

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RESULT 14
AAKS8913/c
ID AAK589
XX AAK589
XX O6-NOV
XX Human
XX Human;
KW Cytost
XX Homo s.
XX Homo 
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Conte: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity
Matches 19; Conserv
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100.0%; Pred. No.
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8.7;
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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent,
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01-DEC-2000
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08 NOV 2000
                                                                                                                                                                                                              Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                      Claim
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P-PSDB; AAM86132.
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diagnosing
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RESULT 15
AAK74060/c
ID AAK74060;
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AAK74060;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
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     2000US-0216880

2000US-0217496

2000US-0218290

2000US-022963

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2000US-022964

2000US-0224518

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2000US-0249211. 2000US-0249212. 2000US-0249213.

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                                                                                                                                       CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to consplement the patients own production of (I). Additionally, (I) CC concern the patients own production of (I). Additionally, (I) CC concern and treat immune/haemstopoletic related diseases, especially CC cancers and cancer metastases of haematopoletic acity eprotein. (I) proteins and polynucleotides may be used to prevent, CC cancers and cancer metastases of haematopoletic related diseases, especially CC cancers and cancer metastases of haematopoletic antigen genomic concerns the present human immune/haematopoletic antigen genomic concerns sequences used in the exemplification of the present invention. AAK54942 to AAK54950 and AAM82169
                                                                         Query Match
Best Local :
                                                         Matches
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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17-NOV-2000;
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17-NOV-2000;
                                                                                                                Sequence 333 BP; 84 A; 91 C; 64 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
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Local
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                                                       4.8%; Solitarity 100.0%; 1
Conservative 0;
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2000US-0256719
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2000US-0249245.
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                                                                      Score 18;
Pred. No.
                                                          Mismatches
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Search completed: January 31, 2003, 03:49:09 Job time: 287 secs

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GenCore version 5.1.3 Compugen Ltd.
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Title:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AUTHORS	SOURCE ORGANIS	RESULT 1 AX245292 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		44	C 42	41		c 38	c 36	3 G		c 32	(6)	c 29	26 27	c 25		221	N N N	c 19			_		. ـ	c 10	_		ი 7 თ	ហ	نا حه	22	Result No.
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o,J., Innis,M.A., inhard,C., Randazz Drmanac,R., Crkven	378 bp atent WO0166753 9966 Chordata; Cran Primates; Cata Pedo,J., Innis, Reinhard,C., R.,	378 bp W00166753.	ALIGNMENTS	AP001352 AC079304	AC007539 HSBA512N4	AC119119	AC016578	AL354828	AC128360	AC097463	AC090625	CNS08CAE AL133389	AC068292	AE006471 AL365259	AL672044	AF339163	BSU39230	AC110152	AC104472	AC009639	AC026210	AP001132 AC124708	AC119775	AC009295	ACUU4520	AL672277	AP004044	AP003087	ACU8418/ AL451145	AL135937	AX245346 AX245370	AX245292 AX245365	ID
Garc1a,P.D., O,F., Kennedy,G.C., Pot,D., jakov,R., Dickson,M.,	Vertebrata; Euteleostomi; ; Hominidae; Homo.	linear PAT 28-SEP-2001		00	ACUU/539 HOMO Sapi AL117341 Human DNA	attu	AC016578 Homo sapi	luman I	attı	AC093330 Raccus no AC097463 Homo sapi	AC090625 Homo sapi	lomo	AC068292 Homo sapi	AE006471 Salmonell AL365259 Human DNA	AL672044 Zebrafish	AF339163 Cynocepha	039230 Bacillus sp	AC110152 Homo sapi		Omo	omo	Mus mus	attu	Mu	ACOU4320 Homo Sapi	Ę.	TYZA	omo s	AL451145 Human DNA	uman DN	equenc	eg	. 3

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	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX245292	VECCUT T
Sudduth-Klinger, J., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M.,	Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D.,	1 (bases 1 to 378)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;	Homo sapiens	human .		AX245292.1 GI:15859966	AX245292	sequence 222 from Patent WO0166753.	AX245292 378 bp DNA linear PAT 28-SEP-2001	•	

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Stache-Crain,B.
Human genes and gene expression products
Patent: WO 0166753-A 222 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
L. .378
                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                         Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Kasaam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
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t: WO 0166753-A 295 13 SEP-2001;
n Corporation (US); Hyseq Inc. (US)
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AX245346.1
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Patent: WO 0166753-A 276 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
Location/Qualifiers
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Mammalia; Eutheria;
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Pred. No. 3.2e-137;
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Best Local Similarity
Matches 232; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAAAACACCCAAGCCGAGTCTCTCACAAGCTTGAATGTGTGTTCTGGAGCTTGAAGGAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAAACACCCAAGCCGGAGTCTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAATCA 298
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                                                                                                      Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 15, 2000 this sequence version replaced gi:7242336.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genes and gene expression products Patent: WO 0166753-A 300 13-SEP-2001; Chiron Corporation (US); Hyseq Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sudduth-Klinger, J., Reinhard, C., Randazzo, F., Kennedy, G.C., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M. Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and
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                  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human DNA sequence from clone
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1 (bases 1 to 59231)
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http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                              Phillimore, B.
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/db_xref="taxon:9606"
63 c 76 g 89
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Pred. No. 1.8e-133;
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n clone RP1-278022 on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
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/note="Charlie4a repeat: matches 25.
7631. .7695
     /note="MIR repeat: matches 169.
complement(15295. .15803)
                                                                                                                                                                                                       /note="L2 repeat: matches 2657. .2750 of consensus" 13719. .13813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2927. .2992
/note="Alu repeat: matches 242. .307 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(10684. .11081)
/note="match: GSS: Em:AQ662878"
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/clone_lib="RPCI-1"
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/chromosome="20"
                                                                                                                                                       137/19. 13813
Noote="12 repeat: matches 2195. .2293 of consensus"
13814. .14087
                                                                                                                                                                                                                                                                                                             12860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="13 copies 2 mer aa 96% conserved"
complement(10684. .11081)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 13. .81 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3880. .4411
/note="LLM4 repeat: matches 4015. .4580 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3019. .3635
/note="L1ME2 repeat: matches 5541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 3. .241 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MER3 repeat: matches 6. .191 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluSq repeat: matches 1. .225 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="LIMC4 repeat: matches 7117. .7739 of consensus"
                                                                              'note="L2 repeat:
                                                                                                                             'note="L1MA5 repeat: matches 6025.
                                                                                                                                                                                                                                                                             note-"match: GSS: Em:AQ035618"
                                                                                                                                                                                                                                                                                                                               'note="L1MA9 repeat: matches 5545.
                                                         .15067
                                                                                                                                                                                                                                                                                                                                                                                                        .11168
                                                                                                                                                                                                                                                   .13423
                                                                                 matches
                                                                                 2078.
                               .262 of consensus*
                                                                                 .2195 of consensus"
                                                                                                                                                                                                                                                                                                                                    .6278 of consensus"
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                                                                                                                                  .6298 of consensus"
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misc_feature
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/note="match:
15961. .16498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="34 copies 2 mer ga 79% conserved"
complement(19364. .19600)
/note="match: GSS: Em:AQ035738"
22132. .22242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MER58B repeat: matches 2. .341 of consensus"
18691. .18717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LTR16C repeat: matches 1. .387 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSg repeat: matches 1.
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18267. .18357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluSx repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                            /note="AluJo repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSq repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="MIR repeat: matches 50. .139 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="LlME3A repeat: matches 5964. .6159 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1ME3A repeat: matches 5427. .5964 of consensus"
                                                      note="MIR repeat: matches 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            te="AluSq repeat: matches 1. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                     e-"MER1B repeat: matches 1.
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                                                                                              e-"MER5A repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e="LIMC4 repeat: matches 7841. .7973 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e-"AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="LTR33 repeat: matches 410.
                                                                                                                                                                                                                                                  e="L2 repeat: matches 1809.
                  e="19 copies 2 mer aa 81% conserved"
                                                                                                                                  -"MIR repeat: matches 191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "56 copies 2 mer ta 73% conserved" .28970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25054
                                                                                                                                                        2 repeat: matches 1420.
34938
                                                                              36273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MC4 repeat:
                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 1945.
                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 2124. .2658 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copies 2 mer ta 68% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 20. .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat:
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                                                                                                                                                                                                                                                                                       repeat: matches 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matches 5678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               matches 7430. .7849 of consensus"
                                                                                                matches 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 5290. .5579 of consensus"
                                                                                                                                                                                                                                                                                                                               .309 of consensus"
                                                        .225 of consensus
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                                                                                                                                    .261 of consensus
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                                                                                                .189 of consensus
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18738

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148 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 207

Indels

0

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18798

208

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   Local Similarity
les 119; Conserv
                                                           44765. .44818
/note="MIR repeat: matches 200. .250 of consensus"
complement(45503. .46337)
                                                                                                       complement(43484 . .44004)
/note="match: GSS: Em:AQ800109"
44765 . .44818
                                                                                                                                                                                                                                                                                                                                                                  /note="L1M3e repeat: matches -879.
39724..39990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 37.
38841. .39254
                                                                                                                                                                                  43333. .43524
                                                                                                                                                                                                  40676. .42726
/note="LlMA9 :
                                                                                                                                                                                                                                  /note="L1MA9 repeat: matches 3999. .4226 of consensus"
40380. .40675
/note="11uJo repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                       39314.
                                                                                                                                                                                                                                                                                                                                                                                                                                         39310. .39339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MSTB repeat: matches 1.
                                                                                                                                                             /note="LTR16C repeat: matches 165.
                                                                                                                                                                                                                                                                                                           /note="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1M3d repeat: matches 251. .280 of consensus"
                                                                                                                                                                                                                                                                                                                                               'note-"L1MA9 repeat: matches 3735.
31.5%; Score 119; DB 9; I
100.0%; Pred. No. 1.6e-62;
^ Mismatches 0;
                                                                                                                                                                                                                                                                                            .40379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .39304
                                                                                                                                                                                                 repeat: matches 4226.
                                                                                                                                                                                                                                                                                                           matches 2. .134 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .150 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .84 of consensus"
                                   Length 59231;
                                                                                                                                                                                                                                                                                                                                               .4011 of consensus"
                                                                                                                                                                                                    . 6308
                                                                                                                                                                                                                                                                                                                                                                                   .779 of consensus"
                                                                                                                                                               .386 of consensus"
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                                                                                                                                                                                                    of.
                                                                                                                                                                                                    consensus"
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LOCUS DEFINITION RESULT 6 AC084187 SOURCE VERSION ACCESSION KEYWORDS ORGANISM

Homo sapiens clone RP11-609K10, AC084187 AC084187.1 GI:10801415 HTGS_PHASEO. DNA linear LOW-PASS SEQUENCE HTG 14-OCT-2000 SAMPLING.

REFERENCE AUTHORS TITLE REFERENCE JOURNAL

AUTHORS

Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McDwan, P., McKernan, K., McPheetters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McDron, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Olivar, T. M., Oliver, J., Peterson, K., Plerre, N., Pisani, C., Pollara, V., Raymond, C., Rleback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thomann, N., Stolanovic, N. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 65118)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-609K10
Unpublished Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkly,L., (bases 1 to 65118)

COMMENT

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Submitted (14-OCT-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  will be sequenced to completion. In the event
the record is updated, the accession number wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This record contains 77 individual sequencing reads that have not been asse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11460
Center clone name: 609_K_10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT
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8445 9198: gap o
9199 9298: gap o
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10148
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1605: contig of 759 bp in length

1606 1705: gap of 100 bp

1706 2465: contig of 757

2466 2565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 9298: gap of 100 bp in 16
99 10047: contig of 749 bp in 16
48 10147: gap of 100 bp
48 10902: contig of 755 bp in 16
103 11002: gap of 100 bp
103 11795: contig of 783 bp in 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 5053: 9-
5818:
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                           17797: gap of
18538: contig
                                                                                                                                           16967:
                                                                                                                                                                                                                     16126:
                                                                                                                                                                                                                                                                                           15308:
                                                                                     1885: gap of 100 bp 11 l 12656: contig of 751 bp 11 l 12736: gap of 100 bp 11 l 13503: contig of 767 bp 11 l 13603: gap of 100 bp 11 l 1457: contig of 754 bp 11 l 1457: gap of 100 bp 11 l 15208: contig of 751 bp 11 l 15308: gap of 100 bp 11 l 15308: gap of 100 bp 11 l 16026: contig of 718 bp 11 l 16026: gap of 100 bp 11 l 16073: cantig of 741 bp 11 l 16673: gap of 100 bp 1 l 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15: gap
4953:
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8344:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 765 bp in length of 100 bn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 760 bp in length of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of.
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contig of 732 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or 100 by contig of 708
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contig of 732 bp in length
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                                                                                                                      corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL451145 65811 bp DNA 1: Human DNA sequence from clone RP11-164A17 on
                                                                                                                                                                                                                                                                                                                                                                                                                                                  requests: clonerequest@sanger.ac.uk
On Jun 11, 2001 this sequence version replaced gi:14268205.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 65811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct
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53350 54084: contig of 735 bp in length
54085 54184: gap of 100 bp
54185 54930: contig of 746 bp in length
54931 5030: gap of 100 bp
55768 55867: gap of 100 bp
55868 5655: contig of 737 bp in length
5656 56755: gap of 100 bp
56756 57500: contig of 788 bp in length
56756 5750: contig of 745 bp in length
57501 57600: gap of 100 bp
58358 58457: gap of 100 bp
58458 59200: contig of 757 bp in length
58358 58457: gap of 100 bp
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50838 51565: config of 728 bp in
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52398 52497: gap of 100 bp
52498 53249: config of 752 bp in
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RR11-164A17 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            true right end of clone RP11-545I5 is at 100 in this sequence
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/note="MER2 repeat: matches 2.
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/note="match: GSS: Em:AQ744388"
complement(1. .100)
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/note="Alusg repeat: matches 1.
10517. .10648
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/note="MER46A repeat: matches 1.
10814. .11006
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                                                  complement(15008...
/note="match: GSS:
complement(19964...
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/db_xref="taxon:9606"
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/note="MER58A repeat: matches 2. .223 of co
11397. .11750
/note="L1M4 repeat: matches 2580. .2953 of
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                                                                                                                                                                                                                                                                                                note-"match: GSS: Em:AQ076115"
                                                                                                                                                                                                                                                                                                                                                                          /note="88 copies 2 mer ta 61% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"match: GSS: Em:B33281"
                                  /note="match:
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copies 2
                                                                     Em: AQ391327"
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mer at 77% conserved"
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complement(21112. .21482)
/note="match: June 121482)
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22125. .22222
  /note="LIME1 repeat: matches 4512.
55395. .55441
                                         /note="L1MEc repeat: matches 1778.
53511..55046
                                                                                                                                 /note="L2 repeat: matches 2254. .2534 of consensus"
32473. .53123
                                                                                                                                                                                                                                                                /note="L1PB3 repeat: matches 5461. .6146 of consensus"
47303. .47470
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12825. .43364
                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluJo repeat: matches 73.
complement(42379. .42834)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39379. .39450
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35192. .35325
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34130. .34477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="15 copies 2 mer tg 86% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-"LIMEC repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note-"MER58 repeat: matches 9. .174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="MER5A repeat:
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23742. .23817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="L2 repeat: matches 2608. .2677 of consensus"
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21335. .21403
                                                                                     'note="LIMEc repeat: matches 1026. .1669 of consensus"
33172. .53433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MLT1B repeat: matches 1. .50 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MIR repeat: matches 186. .258 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MER20 repeat: matches 43. .217 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="L2 repeat: matches 1992. .2327 of consensus" 4804. .35175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluSq repeat: matches 1. .313 of consensus" 1232. .31427 note="AluJo repeat: matches 140. .312 of consensus"
                                                                                                                                                                                                note="MIR repeat:
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5652. .35807
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                                                                                                                                                                                                                                                                                                                                 note="match: GSS: Em:AQ761068"
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                                                                                                                                                                                                                                            te="L2 repeat: matches 2355. .2522 of consensus"
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                                                                                                                                                                                                matches 58. .207 of consensus"
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                                                              .2103 of consensus
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2 (bases 1 to 100403)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
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Homo sapiens genomic DNA, chromosome 11g clone:RP11-594014,
                                                                                                                                                                                                                                                                                                                      On Dec 19,
                                                                                                                                                                                                                                                                                                                                    and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
17-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa
(E-mail:hattoriégsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-JAN-2001) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete sequences.
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                                                                       5.3%; Score 20; llarity 100.0%; Pred. No. Conservative 0; Mismatc
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/note="MER7C repeat: matches 1. .118 of consensus" 55565. .55869
/note="AluY repeat: matches 1. .303 of consensus" 5520
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57945. .58113
                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
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                                                                                                                                                                 /clone="RP11-594014"
20315 c 19157 g
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/note="MER7C repeat: matches 118. .601 of consensus"
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The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* the accession number will be preserved.

* This sequence will be replaced

* the accession number will be preserved.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                      AP005251 129591 bp DNA linear Oryza sativa (japonica cultivar group) chromosome OSJNBb001H15, *** SEQUENCING IN PROGRESS ***, in AP005251
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                                           Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                            Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OSJNBb0011H15.
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  Sasaki,T.,
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/chromosome="8"
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/cultivar="Nipponbare"
  Matsumoto, T. and Katayose, Y
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100.0%;
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC clone:OSJNBb0011H15
Published Only in Database (2002)
2 (bases 1 to 19591)
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (20-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 22, 2002 this sequence version replaced gi:21911559.
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131682 bp DNA linear PRI 20-AUG-2002
Human DNA sequence from clone RP11-309M23 on chromosome X, complete
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                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/db_xref="taxon:39947"
/chromosome="8"
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27555 c 28367 g 37453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence generated from part of bacterial clone contigs of human chromosome x, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
                                                                                                                                                                                 Waterston,R.
Direct Submission
Submitted (01-APR-1998) Department of Genetics, Washington
Submitted (01-APR-1998) Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 132557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 132557)
Sulston, J. E. and Waterston, R.
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                                                                               Direct Submission Submitted (03-FEB-2000) University, 4444 Forest 5 (bases 1 to 132557)
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Dubuque,T., Smith,A., Elliott
The sequence of Homo sapiens
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Homo sapiens BAC clone CTB-119C2 from 7p15, complete sequence
                Direct Submission Submitted (21-FEB-
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/clone_1ib="RPCI-11.2"
31378 c 30235 g 35264
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/db_xref-"taxon:9606"
/chromosome-"X"
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(21-FEB-2002) Department of Genetics, Washington
y, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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Pred. No.
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                                                                                                         Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
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COMMENT
                                                                                                                                                                                                On Feb 21, 2002 this sequence version replaced g1:3004572.
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_RG119C02
                                                                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                            ----- Genome Center
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. all regions were double stranded, This sequence was finished as follows unless otherwise noted: sequenced with an alternate

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nib.gov/DIR/GTB/CHR7, send Clone CTB-119C2 is from the first release of the human BAC 111 CITB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK See: Shizuya et al., Proc. Natl. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. MAPPING INFORMATION: Selection: SOURCE INFORMATION: mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc (http://www.resgen.com). VECTOR: pBeloBAC11 chloramphenicol BAC library Natl. Acad.

NEIGHBORING SEQUENCE INFORMATION:

FEATURES repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region source repeat_region Actual start of this clone is at base position 1 of CTB-119C2; actual end is at base position 132572 of CTB-119C2.

Location/Qualifiers /rpt_family="Alu" /rpt_family="MIR" 3975. .4300 /rpt_family="L2" 2792. .2967 2504. /rpt_family-"L2" 2067. .2202 /rpt_family="Mariner"
571. .607 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="7" /clone-"CTB-119C2" rpt_family-"Alu" /clone_lib-"CITB-978SK-B" rpt_family-"L2" rpt_family="L2" .132557 _family-"Alu" .3454

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                                                                                                                                                                                                 _fami
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                                                                                                                                                                                                                                                                                                                                                    _fami
                                                                                                                                                                                                                                                                                                                                                                        family-"L1"
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                     family-"Alu"
                                                                                                                                  fami
                                                                                                                                                       tami
                                                                                                                                                                          family-"MER1_type"
                                                                                                                                                                                                                                         family-"ERV1"
                                                                                                                                                                                                                                                            family-"MIR"
                                                                                                                                                                                                                                                                                  family-"Alu"
                                                                                                                                                                                                                                                                                                      family-"Alu"
                                                                                                                                                                                                                                                                                                                           ramily-"Alu"
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family="MER1_type"
                                                                                                            fami
                                                                 tami
                                                                                     family-"Alu"
                                          family-"ERVL"
                                                                                                    . 24353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .11817
                                                                                                                       .24034
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16987
                                                               lly-"Alu"
                                                                                                           Lly-"MIR"
                                                                                                                                  Lly-"MIR"
                                                                                                                                                   lly-"MER1_type"
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                                                                                                           JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
AC046149/c
LOCUS
                                                                  COMMENT
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Db 13715 CACAAGCTTGAATGTGTGTT 13696
                                         Query Match
Best Local Similarity
Matches 20; Conserv
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                     84 CACAAGCTTGAATGTGTGTT 103
                                          Conservative
                                                                                                                                                                                                                                                                28341. .28410
/rpt_family="L2"
28546. .28691
                                                                                             7rpt_1
                                                                                                                                                                               30407
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30261
                                                                                                                                                                                                                                             /rpt_fam1ly="MIR" 29423. .29500
                                                                                  /rpt_family-"L1"
                                                                                                                                                                     fami
                                                                                           _family="MIR"
                                                   5.3%; Score 20; 100.0%; Pred. No.
                                                                                                                                               family-"Alu"
                                                                                                                                                                                         family-"Alu"
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                                                                                                                                                                                                     .30406
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                                                                                                                                                            30765
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                                                                                                                                                                    Lly-"Alu"
                                          0
                                         Mismatches
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2;
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                                                             Length 132557;
                                          Indels
                                          0
                                         Gaps
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Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Ferrandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Williamson, A., Ween, Scheng, F., Watlington, S.,
Williamson, F., Watlington, S.,
Watlington, S., Watlington, S.,
Watli Submitted (13-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced gi:11094642. Worley, K.C. Direct Submission Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G., Worley,K. and Gibbs,R. Direct Submission Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 156469) ACO46149 156469 bp DNA linear HTG 16-OCT-2001 Mus musculus chromosome 10 clone RP23-310B11, WORKING DRAFT SEQUENCE, 13 unordered pieces. Unpublished
2 (hasee 1 Mus musculus HTG; HTGS_PHASE1; HTGS_DRAFT. AC046149.5 GI:16118092 (bases 1 to 156469) Genome Center Kelly,S.,

Center: Baylor College of Medicine

Anderson, M.,

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FEATURES
                                                                                                                                                                            RESULT 14
AC009295/c
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   VERSION
KEYWORDS
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                                                                                               DEFINITION
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Best Local Similarity
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NOTE: This is a 'working draft' sequence. It currently
consists of 13 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                                 AC009295 159108 bp DNA linear ROD 01-AUG
Mus musculus chromosome 10, clone RP21-39C4, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length
AC009295.14 GI:9280781
HTG.
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Chemistry: Dye-primer Bodipy: 100% of reads
Chemistry: Dye-primer Bodipy: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 145589 bases at least Q40
Consensus quality: 154088 bases at least Q30
Consensus quality: 157075 bases at least Q20
Consensus quality: 157075 bases at least Q20
Consensus quality: 157075 bases; at least Q20
Consensus quality: 157075 bases; agarose-fp estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.9x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: MAEF center clone name: RP23-310B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129651
136364
136464
142312
142312
147232
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38721
62175
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/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP23-310B11"
38403 c 38896 g 38948 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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62174:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: gap of units
9: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length
contig of 11985 bp in length
gap of unknown length
contig of 11136 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 38620 bp in length contig of unknown length contig of 23454 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 13084 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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of 9668
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bp in length
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bp in l
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Seker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Baker, J., Baldwin, J., Barna, N., Collins, S., Collymore, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Dewon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Donelan, E., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Kann, L., Funke, R., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Funke, R., Beatord, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Melarim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Medarim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Paylin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pietre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lancoque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., McCarthy, M., McDwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McDwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McDwan, P., McGurk, T., Mranda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Feange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zalnoun, J., Zimmer, A. and Zody, M.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus chromosome 10, clone RP21-39C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-AUG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Jul 19, 2000 this sequence version replaced gi:8571747.

All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                   Center project name: L760 Center clone name: 39_C_4
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                                                                                 AC119775 DNA REALTUS norvegicus clone CH230-464J18, *** ***, 61 unordered pieces. AC119775 AC119775.4 GI:21747184 HTG; HTGS_PHASE1.
                       Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
(bases 1 to 162394)
                                                                                                                                                                                                                                                                                  5.3%; Score 20;
nilarity 100.0%; Pred. No.
Conservative 0; Mismatcl
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NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.

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REFERENCE
AUTHORS
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JOURNAL
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Worley,K.C.
Direct Submission
Submitted (02-MAY-2002) Human Genome Sequencing Center, Department Submitted (02-MAY-2002) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced g1:20467838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                Center project information
Center project name: GVOM
Center clone name: GYOM
Center clone name: GYOM
Center clone name: GYOM
Center clone name: CH230-464918
Center summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 112584 bases at least Q30
Consensus quality: 117408 bases at least Q30
Consensus quality: 117408 bases at least Q30
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
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Contact: hgsc-help@bcm.tmc.edu
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as soon as it is available and the accession number will be preserved.
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45206: gap of
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47914: gap of
49906: gap of
51910: contig
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Query Match 5.3%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 2; Matches 20; Conservative 0; Mismatches
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Search completed: January 31, 2003, 04:46:58 Job time : 3388 secs

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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

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Copyright (c) 1993 - 2003 Compugen
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Sequence 23, Appl Sequence 27, Appl Sequence 27, Appl Sequence 289, App Sequence 589, App Sequence 587, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 952, App Sequence 103, App Sequence 103, App Sequence 1004, App Sequence 6004, App Sequence 6004, App Sequence 6004, App Sequence 60035, App Sequence 60035, App Sequence 6001, App Sequence 6021, App Sequence 5980, App Sequence 5980, App Sequence 5980, App Sequence 6021, App Sequence 5980, App Sequence 5980, App Sequence 5980, App Sequence 6021, App Sequence 5980, App Sequence 6021, App Sequence 5980, App Sequence 6021, App Sequence 5980, App Sequence 5980, App Sequence 6021, App Sequen
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	Sequence 3839, Ap		Sequence 41, Appr	Sequence 31349, A	•••	Sequence 131, App	, , ,		ď	4		-	Sequence 37524, A	Sequence 3/523, A	Sequence 3/523, A			Sequence 6011, Ap	Sequence 5980, Ap

ALIGNMENTS

PCT-USO2-10366-23 Sequence 23, Application PC/TUSO210366 GENERAL INFORMATION: APPLICANT: Paddigaru, Muralidhara APPLICANT: Shenoy, Suresh APPLICANT: Shenoy, Suresh APPLICANT: Rekuda, Ramesh APPLICANT: Restelli, Luca APPLICANT: Restelli, Luca APPLICANT: Mezes, Peter APPLICANT: Smithson, Glennda APPLICANT: Guo, Xiaojia APPLICANT: Guo, Xiaojia APPLICANT: Guo, Xiaojia APPLICANT: Guo, Xiaojia APPLICANT: Li, Li APPLICANT: Li, Li APPLICANT: Serhusen, Bryan APPLICANT: Gerhach, Velizar APPLICANT: Gerhach, Velizar APPLICANT: Gerhach, Velizar APPLICANT: Gerhach, Velizar APPLICANT: Malyankar, Uriel APPLICANT: Malyankar, Uriel APPLICANT: Taupter, Raymond J. Jr. APPLICANT: Taupter, Raymond J. Jr. APPLICANT: Taupter, Raymond J. Jr. APPLICANT: Scinder, David APPLICANT: Scinder, Shlomit APPLICANT: Scinder, David APPLICANT: Mazur, Ann APPLICANT: Scinder, David APPLICANT: Scinder, David APPLICANT: APPLICATION NUMBER: PCT/USO2/10366 CURRENT APPLICATION NUMBER: 60/281086 PRIOR APPLICATION NUMBER: 60/281096 PRIOR APPLICATION NUMBER: 60/281096 PRIOR APPLICATION NUMBER: 60/281096 PRIOR APPLICATION NUMBER: 60/281090
plication PC/ TION: Murali ligaru, Murali ligaru, Murali kendy, Suresh kuda, Ramesh stelli, Luca zes, Peter lithson, Glenn o, xiaojia kithson, Glenn o, xiaojia lidog, Ferenc Lithson, Stacie lidog, Ferenc Liturajan, Weliz mgolli, Esha trinet, Corine yrakar, Urie liturajan, Melvyn Jingfang ywan, John kitherion, Elin kitherion, Elin ki
AT BIND TO ANTIGENIC POLYPEPTIDES ANTIGENS, AND METHODS OF USE

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PCT-US02-10366-23
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Best Local Similarity 53.7%;
Matches 73; Conservative
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PRIOR FILING DATE: 2001-04-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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         APPLICANT: Mazur, Ann
TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE ANTIGENS, AND METHODS OF USE
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TYPE: DNA
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DR APPLICATION NUMBER: 60/283444
DR FILING DATE: 2001-04-12
DR APPLICATION NUMBER: 60/283657
DR FILING DATE: 2001-04-13
OR APPLICATION NUMBER: 60/283710
OR FILING DATE: 2001-04-13
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REFERENCE: 21402-322A-061
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                                                                                                      Catterton, Elina
MacDougall, John
Edinger, Shlomit
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Patturajan, Meera
Miller, Charles
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Tchernev, Velizar
Gangolli, Esha
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Guo, Xiaojia
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Kekuda, Ramesh
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                                                                                    Stone, David
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                                                                                                                                                         Peyman, John
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Pred. No. 0.34;
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PCT-US02-10366-27
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PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/281086
PRIOR TILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281906
PRIOR APPLICATION NUMBER: 60/282020
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282030
PRIOR APPLICATION NUMBER: 60/282030
PRIOR APPLICATION NUMBER: 60/282030
                                                                                                                                                                                                                                                                                                       Sequence 27, Application PC/TUS0210366 GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 251\,
                                                                       APPLICANT:
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                    APPLICANT:
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OR APPLICATION NUMBER: 60/283444
OR FILING DATE: 2001-04-12
OR APPLICATION NUMBER: 60/283657
OR FILING DATE: 2001-04-13
OR APPLICATION NUMBER: 60/283710
OR FILING DATE: 2001-04-13
OR FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 TIGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTT 150
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APPLICATION NUMBER: 60/283512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATATAATGTACTGATTTTAACAATGCAGGCCTCACTGCCAAAAGTTCTTCGGTTTTGTGC
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Similarity 53.7%;
Vernet, Corine
Spytek, Kimberly
Malyankar, Uriel
Patturajan, Meera
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Kekuda, Ramesh
Rastelli, Luca
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Casman, Stacie
                                                                     Gangolli, Esha
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Guo, Xiaojia
                                                                                       Tchernev,
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                                                                                                                                                                         Valerie
                                                                                                   Bryan
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Xiaojia

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Remaining Prior Application data removed - Set NUMBER OF SEQ ID NOS: 251
SEQ ID NO 27
LENGTH: 2067
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (93)..(1791)
PCT-USO2-10366-27
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                                                 Sequence 25, Application PC/TUS0210366
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
APPLICANT: Rekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, TITLE OF INVENTION: NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE ANTIGENS, AND METHODS OF USE FILE REFERENCE: 21402-3224-061
CURRENT APPLICATION NUMBER: PCT/US02/10366
CURRENT FILING DATE: 2002-04-03
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PRIOR APPLICATION NUMBER: 60/281086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281906
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
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PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283444
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283657
PRIOR FILING DATE: 2001-04-13
DRIOR FILING DATE: 2001-04-13
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PRIOR FILING DATE: 2001-04-06
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                                                                                                                                                                                                                                                                                                                                    1298 ATATAATGTACTGATTTTAACAATGCAGGCCTCACTGCCAAAAGTTCTTCGGTTTTGTGC
                                                                                                                                                                                                                                                     1358 TIGTGCTGGTATGATT 1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 TTGAATGTGTGTTCTGGAGGTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCCGTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 9.3%;
Local Similarity 53.7%;
es 73; Conservative
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MacDougall, John
Edinger, Shlomit
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Mezes, Peter
Smithson, Glennda
                                     Rastelli,
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                                        Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35.2; DB 1; Length 2067; Pred. No. 0.37; 0; Mismatches 63; Indels 0
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CURRENT APPLICATION NUMBER: PCT/US02/10366
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 10/114153
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/281086
PRIOR APPLICATION NUMBER: 60/281086
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
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                                                                                                                                                                                                                                                                                          NAME/KEY: CDS; LOCATION: (31)..(1645)
PCT-US02-10366-25
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; NUMBER OF SEQ ID N
; SEQ ID NO 25
; LENGTH: 2130
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Best Local S
Matches 73
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FILE REFERENCE: 21402-322A-061
FILE REFERENCE: 21402-322A-061
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PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283710
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
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PRIOR FILING DATE: 2001-04-12
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                     1152 ATATAATGTACTGATTTTAACAATGCAGGCCTCACTGCCAAAAGTTCTTCGGTTTTGTGC
                                                                                                                                   1092 TGGAACCTCTACGCTCTTGGTTTGGGTTGGAGTCATCAGATACCTGGGTTATTTCCAGGC 1151
211 TCAACATGCTTTGACT 226
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                                                                                                                                                                                                                  Local Similarity 53.7
les 73; Conservative
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                                                                                            GTTTAATCTAATGTTCTTTGGAATAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGC 210
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Spytek, Kimberly
Malyankar, Uriel
Patturajan, Meera
Miller, Charles
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Casman, Stacie
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MacDougall, John
Edinger, Shlomit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application data removed - See File Wrapper or PALM
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                                                                                                                                                                                                                     Score 35.2; DB
Pred. No. 0.37;
); Mismatches
                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                           Length 2130;
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1212 TTGTGCTGGTATGATT 1227

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; TYPE: DNA
; ORGANISM: Homo saplens
US-10-276-774-299
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                                                                                                   COURRENT APPLICATION NUMBER: PCT/US02/38526
COURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR APPLICATION NUMBER: PCT/US00/34263
PRIOR APPLICATION NUMBER: PCT/US00/34263
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-26
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Best Local S
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APPLICANT: Mulero, Julio J
APPLICANT: Boyle, Bryan J.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUCI
FILE REPERENCE: HYS-B1/PCT
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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CURRENT FILING DATE: 2002-11-18
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APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 492
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                                                                             APPLICATION NUMBER: US 09/496,914
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                                    CATION NUMBER: US 09/560,875
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Wang, Zhiwei
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                                                             2000-02-03
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PCT/US01/03800
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Best Local Similarity
Watches 72; Conserve
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PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-23
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: PCT/US00/34263
PRIOR APPLICATION NUMBER: PCT/US00/34263
PRIOR FILING DATE: 2000-12-26
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NUMBER OF SEQ ID NOS: 653
SOFTWARE: PatentIn version 3.1
SEQ ID NO 589
                   SOFTWARE: Pate
SEQ ID NO 587
LENGTH: 1640
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PRIOR APPLICATION NUMBER: US 09/598,075
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APPLICANT: Boyle, Bryan J.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POI
FILE REFERENCE: HYS-B1/PCT
CURRENT APPLICATION UNUBER: PCT/US02/38526
CURRENT FILING DATE: 2002-12-03
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                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                     Remaining Prior Application data removed
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TYPE: DNA
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APPLICATION NUMBER: PCT/US01/03800
APPLICATION NUMBER: US 09/598,075
                                                                                                                                                                                                                                                        FILING DATE: 2000-02-03
APPLICATION NUMBER: US 09/560,875
                                                                                                                                          FILING DATE: 2000-06-20
APPLICATION NUMBER: PCT/US01/04098
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Zhao, Qing
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Wang, Jian-Rui
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Pred. No. 1
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Query Match
Best Local Similarity
Thes 72; Conserve
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SOFTWARE: Patent.pm
SEQ ID NO 33882
LENGTH: 158
                                                                                                             Sequence 7, Application PC/TUS0232700 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
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                                                              APPLICANT:
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LOCATION: (1)..(16
OTHER INFORMATION:
                                                APPLICANT:
                                                                                              APPLICANT: Keith, Tim
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   INVENTION:
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             Van Eerdewegh, Paul
Dupuis, Josee
Del Mastro, Richard (
Allen, Kristina
                                                                               Little, Randall D.
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NUCLEOTIDE AND AMINO ACID SEQUENCES
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Pred. No. 1.1;
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Pred. No. 0.6;
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US-10-271-416-7
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                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/271,416
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/328,424
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ: ID NO 7
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GENERAL INFORMATION
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Best Local Similarity
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                                                   Query Match
Best Local Similarity
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CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/328,424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(45450)
OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(45450)
OTHER INFORMATION: n =
                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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 133 CCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAG 192
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                                                                                                                                                                                                                                                                                                                                                                                                               Allen, Kristina
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Del Mastro, Ri
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                                                                                                                       A,T,C
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                                   Score 32.6; DB pred. No. 6.7; 0; Mismatches
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Pred. No. 6.
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SEQ ID NO 5935

LENGTH: 334

TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: jC-gmf102220076bl1a1
US-09-531-113-5935
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GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr.
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TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION NUMBER: US/09/531,113
CURRENT FILING DATE: 2000-03-22
                                                                        APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/1C963US2
CURRENT APPLICATION NUMBER: US/09/950,084
CURRENT FILING DATE: 2001-09-10
CURRENT FILING DATE: 2001-09-10
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                     PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: US 09/417,811
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Pred. No. 1.6;
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; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-950-084-952
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                                                                                                     ; LOCATION: 388
; OTHER INFORMATION: n=a,
US-09-513-999C-30304
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SEQ ID NO 952
LENGTH: 264
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Matches
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SEQ ID NO 30304
LENGTH: 410
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                                                                      Query Match
                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 36681
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LOCATION: 387
OTHER INFORMATION: v-a
                                                                                                                                  NAME/KEY: misc_feature LOCATION: 388
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                                                                                                                                                                     FEATURE
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                                                                                                                                                                                                                                                                 TYPE: DNA
196 TACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGA 255
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nes 52; Conserv
                                                     Local Similarity
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APPLICATION NUMBER: US 09/036,720
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                                 Conservative
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Pred. No. 1.7;
                                                     Score 32;
Pred. No.
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                                 Mismatches
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390 TANBTACTCTCATTCTCAAAAGCCAGGCATTCATAAATGTGGAGCTATGTCTTTTTCTGA 331

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APPLICANT: Secrit, Heather

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

FILE REFERENCE: 210121.426C12

CURRENT APPLICATION NUMBER: US/10/294,443

CURRENT FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 243

SOFTWARE: FRASESEQ for Windows Version 3.0

SEQ ID NO 103

LENGTH: 2966

TYPE: DNA

ORGANISM: Babesia microti
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                  SEQ ID NO 112
LENGTH: 3011
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 112, Application US/10294443 GENERAL INFORMATION:
                                                                                                                                                                   APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: Sleath, Paul R.

APPLICANT: McNeill, Patticia D.

APPLICANT: Homer, Mary J.

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

FILE REFERENCE: 210121.426C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                               CURRENT APPLICATION NUMBER: US/10/294,443
CURRENT FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 243
SOFTMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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ORGANISM: Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 TATTCTACTTTTAATATAATTTTTTATTCAATAATAATACTCTTTCAATATTTTGTACTAT 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 AGGGATGGTGATGGAGAFGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 GATGATATACATGAATATGCAT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 GGTGATGGAGATGCCAATCCAT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 TITATATAATCATATATATATATATATATATATATATTGATAATTGAATATATCAATAAT 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watch 8.4%;
Local Similarity 51.4%;
Local Similarity 51.4%;
Local 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31.6; DB 6;
Pred. No. 5.8;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69; Indels
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Best Local Similarity 51.4
Matches 73; Conservative
                                                                                                                                                      142 TTTTCCGTTGTTTAATGTTATGTTCTTTGGAATAAAACCTCCCTGCCAAGTAGTACTTG 201
                                                                331 TTTATATAATCATATATATATATATATATATATATTTTGATAATTGAATATATCAATAAT 390
                                                                                                                                    271 TATTCTACTTTTAATATAATTTTTTTATTCAATAATATACTCTTTCAATATTTGTACTAT 330
391 GATGATATACATGAATATGCAT 412
                               262 GGTGATGGAGATGCCAATCCAT 283
                                                                                                202 GTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT 261
                                                                                                                                                                                                                       8.4%;
                                                                                                                                                                                                       Score 31.6; DI Pred. No. 5.8; 0; Mismatches
                                                                                                                                                                                                                                      DB 6; Length 3011;
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Search completed: January 31, 2003, 01:19:25

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-803-719-222
378
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Copyright (c) 1993 - 2003 Compugen
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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APPLICANT: WILLIAMS, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Innis, Michael A.
APPLICANT: Innis, Michael A.
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Reinhard, Christoph
APPLICANT: Randazzo, Filippo
APPLICANT: Randazzo, Filippo
APPLICANT: Kassam, Altaf
APPLICANT: Lamson, George
APPLICANT: Lamson, George
APPLICANT: Lingon, Mark
APPLICANT: Dickson, Mark
APPLICANT: Lingon, Mark
APPLICANT: Lingon, Secana
APPLICANT: Lingon, Secana
APPLICANT: Lingon, Wiltz, Dena
APPLICANT: Lingon, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache
                                                                   ; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-803-719-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-09-803-719-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 222, Application:
            Query Match
Best Local Similarity
Matches 378; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09803719
               Conservative
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21 US-09-552-086-14635
22 US-09-552-086-14635
23 US-09-874-708A-88442
25 US-09-874-708A-82309
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21 PCT-US01-10366-27
21 US-09-86-25-6548
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24 US-09-634-306B-256548
25 US-10-027-632-256548
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               0;
          Score 378; DB 31,
Pred. No. 3.8e-106;
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                                      Length
               Indels
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Sequence 363, App
Sequence 83442, A
Sequence 8230, Appl
Sequence 23, Appl
Sequence 21, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 25, Appl
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Sequence 30211, A
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; NAME/KEY: CDS
; LOCATION: 84..404
US-09-621-976-3594
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US-09-621-976-3594
; Sequence 3594, Application US/09621976
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SOFTWARE: Patent.pm
SEQ ID NO 3594
LENGTH: 512
TYPE: DNA
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human
FILE REFERENCE: GENSET.054PR2
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Matches
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CURRENT FILING DATE: 2000-07-21
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                                       TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTTGGCACACTTGAAGGGATGGTGAT
Conservative
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Pred. No. 6.3e-95;
O; Mismatches 5;
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GGAGATGCCAATCCATGGAATCAGGTGGCACAGCTATGTTGGTAGCTATAGCAGAAGTCT

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CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTMARE: PALENT.pm
SEQ ID NO 8066
LENGTH: 512
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US-09-834-366-8066
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Sequence 3594, Application US/60147499
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Prile REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/60/147,499
CURRENT FILING DATE: 1999-08-05
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US-09-834-366-8066
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US-60-147-499-3594
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Best Local Similarity 98.6%;
Matches 345; Conservative
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
TITLE OF INVENTION: ESTs and Encoded Human Prot
FILE REFERENCE: 81.USZ.REG
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ORGANISM: Homo sapiens
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Pred. No. 6.3e-95;
0; Mismatches 5;
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; FEATURE:
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; LOCATION: 84..404
US-60-147-499-3594
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SOFTWARE: Patent.pm
SEQ ID NO 3594
LENGTH: 512
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; LOCATION: 84..404
US-60-197-873-8066
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Best Local :
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Best Local S
Matches 345
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SOFTWARE: Patent.pm
SEQ ID NO 8066
LENGTH: 512
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.US1.PRO
CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
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                                                                                                                                                                     LENGTH: 512
TYPE: DNA
ORGANISM: Homo sapiens
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AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCC 147
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Jobert, Severin
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Tanaka, Hiroaki
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Pred. No. 6.3e-95;
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                                                                           Score 342; DB 63;
pred. No. 6.3e-95;
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PRIOR APPLICATION NUMBER: 60/188,609
: PRIOR FILING DATE: 2000-03-09
: NUMBER OF SEQ ID NOS: 2396
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 276
: LENGTH: 327
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-803-719-276.
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APPLICANT:
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APPLICANT:
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APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
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CURRENT FILING DATE: 2001-03-09
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                           AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCC 140
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                                                                                                                                             h 79.3%;
Similarity 98.7%;
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Dickson, Mark
Drmanac, Snezana
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Kita, David
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Drmanac, Radoje
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Kennedy, Giulia
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Sudduth-Klinger, Julie
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                                                                                                                                            Score 299.6; DB 3
Pred. No. 7.5e-82;
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ORGANISM: Homo sapiens
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; NAME/KEY: misc_feature
; LCCATION: (1)...(322)
; OTHER INFORMATION: n = A,T,C
US-09-803-719-295
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SEQ ID NO 295
LENGTH: 322
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CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEO ID NOS: 2396
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APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
                                                                                                         GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 207
                                  AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCC
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Kita, David
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Crkvenjakov, Radomir
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Kennedy, Giulia C.
Pot, David
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98.6%;
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Pred. No. 1.2e-75;
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US-09-803-719-300
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SEQ ID NO 300
LENGTH: 318
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CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
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TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
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268 GGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGT 310
                                                          208 TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT 267
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                                                                                                         GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 207
                                                                                                                                                AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCC 147
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                             TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT 275
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Jones, Lee William
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Garcia, Pablo Dominiquez
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Pred. No. 3.2e-74;
0; Mismatches 5;
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APPLICANT: Wattler, Sigrid
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
ITILE OF INVENTION: Novel Human Polynucleotides and
ITILE OF INVENTION: US/09/718,457
CURRENT APPLICATION NUMBER: US/09/718,457
CURRENT FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: US 60/167,870
FILING DATE: 1999-11-29
NUMBER OF SEO ID NOS: 1008
SEO ID NO 565
LENGTH: 562
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-718-457-565
                                                                                     ; ORGANISM: Homo sapiens US-09-534-844A-5172
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                                                                                                                                        NUMBER OF SEQ ID NOS: 14510
SOFTWARE: Hy patent pl Version 1.1
SEQ ID NO 5172
LENGTH: 403
TYPE: DNA
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various CNA Libraries FILE REFERENCE: 21272-109 (775)
CURRENT APPLICATION NUMBER: US/09/534,844A
CURRENT FILING DATE: 2001-03-24
PRIOR APPLICATION NUMBER: 60/126,605
PRIOR FILING DATE: 1999-03-26
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birg:
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stache-Crain, Birgit
Dickson, Mark C.
Jones, Lee W.
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  34.78;
95.78;
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  Score
Pred.
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Pred. No. 3.5e-59;
  131; DB 20;
No. 1.6e-29;
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APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Polynucleotides and the
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: LEX-0064-USA
CURRENT APPLICATION NUMBER: US/09/689,907
CURRENT FILING.DATE: 2000-10-11
PRIOR APPLICATION NUMBER: US 60/158,799
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEO ID NOS: 1508
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 861
LENGTH: 524
TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-689-907-861/c
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APPLICANT: Harrington, John J

APPLICANT: Jackson, P. David
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                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 19036
                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                     APPLICANT: Ramachandran, Rakesh
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS
FILE REFERENCE: ATX-001CN
CURRENT APPLICATION NUMBER: US/10/098,754
CURRENT FILING:DATE: 2002-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nehls, Michael
                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/791539 PRIOR FILING DATE: 2001-02-22
                                                                                                                                NUMBER OF SEQ ID NOS: 21107
                                                                                                                                                                                                                                                                                     APPLICANT:
                            LENGTH: 806
TYPE: DNA
ORGANISM: Homo saplens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 AAGTCTTCTTGGCAAAGATTCCTCC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 AAGTCTTCTTGGCAAAGATTCCTCC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 GGTGATGGAGATGCCAATCCATGGAATCAGGTGGCACAGCTATGTTGGTAGCTATAGCAG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 GGTGATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGCAG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84;
                                                                                                                                                                                                                                                                                                                         Sherf, Bruce A.
                                                                                                                                                                                                                                                                                                         Cain, Scott
                                                                                                                                                                                                                                                                                     Rundlett, Stephen E.
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llarity 98.8%;
Conservative
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Pred. No. 1e-14;
0; Mismatches 1;
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TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: LEX-0055-USA
CURRENT APPLICATION UNMER: US/09/685,045
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/158,741
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1053
LENGTH: 125
TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: (1)...(806)
; OTHER INFORMATION: n =
US-10-098-754-19036
                                                                                                                                                                       RESULT 14
US-09-362-510-51216
; Sequence 51216, Application US/09362510
; GENERAL INFORMATION:
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US-09-685-045-1053
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Matches
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Best Local Similarity
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE EFFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362,510
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 09/221,820
EARLIER APPLICATION NUMBER: 1998-12-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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NAME/KEY: misc_feature
LOCATION: (1)...(125)
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                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 103; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          GGGATGGTGATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTAT 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zambrowicz, Brian
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Pred. No. 2.2e-13;
0; Mismatches 1;
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RESULT 15
US-09-362-510A-51216
Sequence 51216, Application US/09362510A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362,510A
CURRENT APPLICATION NUMBER: US 09/221,820
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 09/221,820
VAMBER OF SEQ ID NOS: 62165
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51216
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(381)
OTHER INFORMATION: n - A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / NVMBER OF SEQ ID NOS: 62165
// SOFTWARE: FastSEQ for Windows Version 3.0
// SEQ ID NO 51216
// LENGTH: 381
// TYPE: DNA
// ORGANISM: Homo sapiens
// FEATURE:
// NAME/KEY: misc_feature
// LOCATION: (1)...(381)
// OTHER INFORMATION: n = A,T,C or G
US-09-362-510-51216
Search completed: January 31, 2003, 02:17:22 Job time : 3495 secs
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Best Local Similarity
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Best Local Similarity 96.2%;
                                                              326 CTTCTTGGCAAAGATTCCTCCCGGGAAGGAAGGTACCATTGGAGAACCATGC 377
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                                                                                                                                     12.9%;
nilarity 96.2%;
Conservative
                                                                                                                                 Score 48.8; DB 17;
Pred. No. 0.00049;
0; Mismatches 2;
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                                                                                                                                                                      Length 381;
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                                                                                                                                     0,
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      seg length: 0 seg length: 2000000000
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: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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               9 US-09-938-842A-3096

10 US-09-737-178-103

10 US-09-737-178-112

9 US-09-286-488-10

10 US-09-737-178-12

10 US-09-737-12790

10 US-09-736-692-4354

10 US-09-796-692-4354

10 US-09-796-892-4354

10 US-09-796-892-4354

10 US-09-796-817-2678

10 US-09-786-847-2678

10 US-09-822-849A-246

10 US-09-822-849A-246

10 US-09-823-867-1518

10 US-09-818-512-3

10 US-09-783-590-12445

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10 US-09-783-590-12445

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10 US-09-783-590-12445
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Sequence 3096, Ap
Sequence 112, Appl
Sequence 110, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 204, Appl
Sequence 204, Appl
Sequence 2678, App
Sequence 2678, Appl
Sequence 1518, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
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10 US-09-813-320-3	10 US-09-880-107-2380	10 US-09-764-877-2322	9 US-09-754-853A-3	9 US-09-754-853A-2	10 US-09-358-082A-29	9 US-10-008-016-1	9 US-10-008-016-3	10 US-09-742-312-3		10 US-09-070-927A-351	9 US-09-938-842A-448	10 US-09-822-830A-312	10 US-09-782-953-17	10 US-09-954-456-497				9 US-09-928-457-97		10 US-09-826-212-1	10 US-09-887-879-4	10 US-09-887-879-2	9 US-09-992-964-4	9 US-09-992-964-2	12 US-10-044-090-150
Sequence 3, Appli	Sequence 2380, Ap	Sequence 2322, Ap	Sequence 3, Appli	Sequence 2, Appli	Sequence 29, Appl	Sequence 1, Appli	Sequence 3, Appl1	Sequence 3, Appli	13,	Sequence 351, App	Sequence 448, App	Sequence 312, App	Sequence 17, Appl	Sequence 497, App	Sequence 18, Appl	Sequence 81, Appl	Sequence 1477, Ap	Sequence 97, Appl		Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 150, App

ALIGNMENTS

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APPLICANT: KIRPS, JOE1
APPLICANT: KIRPS, JOE1
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIN)
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3096
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US-09-938-842A-3096
Sequence 3096, Application US/09938842A
Patent No. US20020160378A1
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Best Local S
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                    362 GGAGACCATATATGGACTTCTGGAACTCCGCTTAACATATCTCTCGTGTACACACATGCG 421
482 AGTTAAACGTAAAGCTTTATTAAACAAAGAACAAAT 517
                                                                                                  106 GGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTT 165
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                                                                                                                                  CTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGAC
                                               TGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT 261
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RESULT 2 US-09-737-178-103

Application US/09737178

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; SOFTWARE: FastSEQ for Windc
; SEQ ID NO 112
; LENGTH: 3011
; TYPE: DNA
; ORGANISM: Babesia microti
US-09-737-178-112
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                                          Query Match
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Best Local :
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    Matches
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEO ID NOS: 144
                                                                                                                                                                                             FILE REFERENCE: 210121.426C9
CURRENT APPLICATION NUMBER: U2/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
                                                                                                                                                                                                                                                 APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
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  Local Similarity 51.4 hes 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGATATACATGAATATGCAT 412
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                                                                                                                                                                               FastSEQ for Windows Version 3.0
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Lodes, Michael J.
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                    8.4%; Score 31.6;
51.4%; Pred. No. 4
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    Mismatches
                                        DB 10;
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; ORGANISM: Babesia microti
US-09-286-488-10
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APPLICANT: Reed, St
APPLICANT: Lodes, M
APPLICANT: Houghton
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CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09737178 Patent No. US20010029295A1
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Best Local Similarity 51.4%;
Matches 73; Conservative
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C3
CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 83
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                                                                                                                             APPLICANT: Sleath, Paul R.
APPLICANT: MCNeill, Patricia D.
APPLICANT: HOMET, MATY
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
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                            for Windows Version 3.0
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 Mismatches

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; TYPE: DNA
; ORGANISM: Babesia
US-09-737-178-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12790, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
                                                                                                 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENCTH: 3701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      999 TATTCTACTTTTAATATATTTTTTTTTTCAATAATATACTCTTTCATATTTTGTACTAT 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 TTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTG 201
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                   APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGATATACATGAATATGCAT 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT
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nilarity 51.4%;
Conservative
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Pred. No. 4.
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; Sequence 4354, Application US/09796692
publication no. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
                                                                       RESULT 8
US-09-796-692-4354/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49, Application US/10002344A
Patent No. US20020172959A1
GENERAL INFORMATION:
APPLICANT: Recipon, Herve
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LENGTH: 568
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                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: Chen, Sel-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0241
CURRENT APPLICATION NUMBER: US/10/002,344A
CURRENT FILING DATE: 2002-03-15
CURRENT FILING DATE: 2002-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 631
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO ACO11260.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.94

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                             563
                                                                                                                                                                166 CTTTGGAATAAAAA 179
                                                                                                                                                                                                                   623
                                                                                                                                                                                                                                                    106
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                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 GAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGT 152
                                                                                                                                                                                                                                                    GGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTT 165
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                                                                                                                                                                                                                   GCAACTGAAGGGCTAACATTTATTGAGCCCCTTCTTTTTTGCCATGATCTTTGATATGTG 564
                                                                                                                                                                                                                                                                                       47;
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47; Conserv
                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                      8.1%;
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Pred. No. 4
                                                                                                                                                                                                                                                                                       Mismatches
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APPLICANT:

Algate, Paul A.

APPLICANT:

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RESULT 9
US-09-745-763-204
: Sequence 204, Application US/09745763
: Patent No. US20020065394A1
: GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-796-692-4354
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SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/186,126 PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY ITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES (LE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 TTTACATATATGCAGGGAAGTAATGGTACTGGTAGTGTATGTTTTCTATGTGGTTCAA 276
                                                                                                                                                                                                                                                                                                                                                                     215 GTCACAACCAAATTGAT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 AGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAATCAGGT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 TAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 ATGCTGCGTTGTTCAGCAGCCCCCCTGTGTTTTGTGTGATTTGTTTTATTTTTCCTTTTT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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FILING DATE: 2000-08-04
APPLICATION NUMBER: 60/223,378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/200,303 FILING DATE: 2000-04-28 APPLICATION NUMBER: 60/200,779 FILING DATE: 2000-04-28
                                                                                                                                                                                            APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/206,201 FILING DATE: 2000-05-22
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FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/
FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATGAATTTCGAACACACCAAGCCGCTAATGAGATAGCAGCTTTTTTCTGGGACCCAGA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 47.2%;
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        Treacy, Maurice Spaulding, Vikki INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                        Collins-Racie, Lisa
Evans, Cheryl
                                                                                                                                              McCoy, John M.
LaVallie, Edward R.
                                                                               Merberg, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-08-07
ENCODING
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Pred. No. 3.9;
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THEM
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                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2678
LENGTH: 26591
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                                                                                                                                                                                                                                                                                                                Sequence 2678, Application US/09764877
Patent No. US20020147140A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
      TYPE: DNA
ORGANISM: Homo sapiens
-09-764-877-2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/764,877 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                             APPLICANT: Rosen et al. TITLE OF INVENTION: Nuc FILE REFERENCE: PC005
                                                                                                                                       Prior application data removed - NUMBER OF SEQ ID NOS: 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 204
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                3118 GTCACAACCAAATTGAT 3134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3058 ATATGAATTTCGAACACACCAAGCCGCTAATGAGATAGCAGCTTTTTTCTGGGACCCAGA 3117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 GGCGCAGCTATGTTGGT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 AGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 204:
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REGISTRATION NUMBER: 41.323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8384
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGACCTTTGGCACACTTGAAGGGATGGTGATGGAGATGCCAATCCATGGAATCAGGT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93;
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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ilarity 47.2%;
Conservative
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Pred. No. 1:
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DB 10;

Indels Length 4285;

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Gaps

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; ORGANISM: Homo sapiens
US-09-822-849A-246
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Best Local S
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SEQ ID NO 246
LENGTH: 2648
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Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1518
LENGTH: 1655
                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                          Sequence 1518, Application US/09764847 Patent No. US20020132767A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/822,849A CURRENT FILING DATE: 2001-09-04 PRIOR APPLICATION NUMBER: 60/195,582 PRIOR FILING DATE: 2000-04-06 NUMBER OF SEQ ID NOS: 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 8.0%;
Local Similarity 51.5%;
hes 70; Conservative
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Agostino, Michael J.
Howes, Steven H.
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58.1%;
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Pred. No. 10;
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Pred. No. 24;
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US-09-818-512-3/c
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GENERAL INFORMATION:

APPLICANT: BEASLEY, Ellen et al.

TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS,

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN E

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001192

CURRENT APPLICATION NUMBER: US/09/818,512

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                             Sequence 3, Application US/09818512 Patent No. US20020142416A1
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Best Local
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NAME/KEY: CDS
LOCATION: (3639)...(3984)
NAME/KEY: CDS
LOCATION: (11757)...(12601)
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APPLICANT: Johannsdottir, Vala Drofn
TITLE OF INVENTION: Human Osteoporosis Gene
FILE REFERENCE: 2345.2009-001
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PRIOR FILING DATE: 2000-09-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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TYPE: DNA
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nes 78; Conservative
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Pred. No.
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: LOCATION: (1)...(116592)
; OTHER INFORMATION: n = A,T,C
US-09-818-512-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-783-590-12445
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PATENTIN VER. 2.0
SEQ ID NO 12445
LENGTH: 438
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2

FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 08/420,856 PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/783,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dillon, Patrick J.
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                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (177)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (276)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (345)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (333)
OTHER INFORMATION: n equals a,t,g,
                                                                  NAME/KEY: misc feature
                                                                                    OTHER INFORMATION: n equals
                                                                                                            NAME/KEY: misc feature LOCATION: (335)
                                                                                                                                             OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (334)
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTAACTAATAAATGGTCTGTGGATAGGAAAGACCCCAAAGTAGCATAGCACAGTCTTTGA 20064
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Similarity 49.4%;
78; Conservative
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Li, Haodong
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Pred. No. 70;
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; LOCATION: (422)
OTHER INFORMATION: n equals a,t,9, or
; NAME/KEY: misc feature
; LOCATION: (429)
; OTHER INFORMATION: n equals a,t,9, or
US-09-783-590-12445
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Search completed: January 31, 2003, 01:17:11 Job time: 157 secs
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Best Local Similarity 61.0%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (407)
OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                                                         150 GAATGTGTGTTCTGCAGCTGATGGATGNAATGTTTTGTAAATGTCTGTTAGATCCATTTA 209
                                                                                                                                                                              93 GAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGT 152
                                                                                                                   TTAATCTAATGTTCTTT 169
                                                                                                                                                                                                                                                         Score 29.6; D
Pred. No. 8.1;
                                                                                                                                                                                                                                        Mismatches
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GenCore version 5.1.3 Compugen Ltd
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Run on: OM nucleic - nucleic search, using sw model

January 30, 2003, 23:50:38; Search time 52 Seconds (without alignments) 2229.304 Million cell updates/sec

Title: Perfect score: US-09-803-719-222 378

1 tacggctgcttaagacgact.....taccattggagaaccatgcg 378

Scoring table: Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 882724

441362 segs, 153338381 residues

Searched:

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA: *

Database

/cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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28.8	28.8	29	29.2	29.2	29.2	29.2	29.2	٠	29.2	•	29.4	29.4	29.4	29.4	29.4	29.4	29.6	29.6	29.6	•	30	30.4	31.6	31.6	31.6	31.6		2019
7.6	7.6	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	٠		7.9		8.4	8.4	8.4	8.4		Query
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US-08-504-718D-14	US-08-504-718D-13	US-09-345-882-1	PCT-US95-02520-2	US-08-796-364-2	US-08-660-754-2	US-08-204-675-2	PCT-US95-02520-3	US-08-796-364-3	754-	US-08-204-675-3	5217870-1	US-08-482-073-1	US-09-009-490A-88	US-08-344-155C-98	US-08-365-470-1	US-09-209-668-18	ڄ	-09-	-09-	US-09-134-618-3	-08-378-548-2	-09-593-995-1	-784A-	-142A	US-08-990-571-10	US-08-845-258-10	· · · · · · · · · · · · · · · · · · ·	.
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1 US-08-504 718D-16 4 US-09-017-754A-19 1 US-07-828-700-7 1 US-09-134-001C-1029 1 US-08-981-803-9 3 US-08-981-803-9 3 US-08-983-440-9 4 US-09-983-440-23 4 US-09-983-440-23 4 US-08-983-440-23 5 US-08-983-440-23 2 US-08-981-803-29 3 US-08-981-803-29 3 US-08-981-803-29 4 US-08-981-803-29 4 US-08-981-803-29 5 US-08-981-848-3 2 US-08-951-648-5 3 US-08-951-648-5 3 US-08-951-648-5	4389	3195	3195	2298	2298	11478	11478	699	376	376	376	. 376	1068	2358	2259	1205	420	
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ALIGNMENTS

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US-08-845-258-10
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 Query Match
Best Local Similarity
Matches 73; Conserv
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                                                                                                                                                                                                      APPLICATION NUMBER: US/08/845,258
APPLICATION 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mak1, Dav1d J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                           TELEFAX: (206)682-603: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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6300 Columbia Cent
                                                                                                                                                                         (206)682-6031
(207) TD NO: 10:
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Houghton, Raymond
Sleath, Paul R.
   8.4%;
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Conservative
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Score 31.6; DB Pred. No. 1.6; 0; Mismatches
     0;
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                                     Length 3701;
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RESULT 3
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                                                    Sequence 10, Application US/08723142A Patent No. 6306396
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                        Matches
                       GENERAL INFORMATION: APPLICANT: Reed,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Reed, St
TITLE OF INVENTION:
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NAME: Mak1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION INFORMATION:
           APPLICANT:
                                                                                                                                                                                                      1059 TTTATATAATCATATATATTATATAATTATATATATATTTGATAATTGAATATATCAATAAT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 11-DEC-19
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                       142 TTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAACCTCCCTGCCAAGTAGTACTTG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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73; Conserv
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DEDNESS: single
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6300 Columbia Center, 701 Fifth Avenue
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        Reed, Steven G
Lodes, Michael
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US-09-528-784A-10
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US-08-723-142A-10
                          SOFTWARE: FastSEQ
SEQ ID NO 10
                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Reed, St
                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                               APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.425C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                      CURRENT APPLICATION NUMBER: US/09/528,784A CURRENT FILING DATE: 2000-03-17 NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                     APPLICANT:
TYPE: DNA
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انام ، 645131
اسم میران
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                                                                                                                                                                                                                   Steven G.
                                         Windows Version 3.0
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TELEFAX: (206)682-603: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILLING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
999 TATTCTACTTTTAATATATTTTTTTATTCAATAATATACTCTTTCATATTTTGTACTAT 1058
                      142 TTTTCCGTTGTTTAATCTTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTG 201
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                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                           Conservative
                                                                                                                                                                                                                                                                     (206)682-6031
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SYSTEM: PC-DOS/MS-DOS
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                                                                                          Score 31.6;
Pred. No. 1.
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                                                                     Mismatches
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ORGANISM: Babesia microti

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; ORGANISM: Homo sapiens
US-09-593-995-10
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Best Local
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Best Local Similarity 51.4%;
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CURRENT FILLNG DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/139,121
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
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                                                                                                                                                                                                         APPLICANT:
                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                         TITLE OF INVENTION: Protein Fusion Method and Constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 TTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTAT 208
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COMPUTER READABLE FORM:
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mes 64; Conserv
                                                CITY: Chicago
STATE: Illinois
                                                                                   STREET:
                              COUNTRY:
                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                           INFORMATION:
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                   60606
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Gao, Zeren
                                                                                  E: Banner & Allegretti, Ltd
Ten South Wacker Drive
                                                                                                                                                                      Weber, J. Mark
Gaines III, George L.
                                                                                                                                                                                                        Casadaban,
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Pred. No. 1.6;
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; LOCATION: (1)..(897)
US-09-134-618-3
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US-09-134-618-3/c
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Best Local Similarity
Matches 54; Conserv
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SEQ ID NO 3
LENGTH: 900
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                                                                                                                                                        Query Match
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                                                                                                                       Matches
                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 480140.432
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/134,618 CURRENT FILING DATE: 1998-08-14
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 6
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3449 GAAAGCCCGCTCTCAAGAGCAATTTGTTTAAAGG 3416
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA REPLICATION DATA:
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LENGTH: 7003 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Chao, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                               120 CACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 AAAACCTCCCTGCCAAGTAGTACTTGGTTTTATG 209
                                                429 CATGGTGCAGGAACTTTTATGTTTTTGATCTGATTTACAAACTGTACATGGGAAGCAAGA 370
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              180 CCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGAC 239
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OTHER INFORMATION: /not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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DEDNESS: both
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                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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48.3%;
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                                                                                                                                       Score 29.6; DI
Pred. No. 3.7;
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                                                                                                                       Mismatches
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                                                                                                                                                        DB 4; Length 900;
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US-09-006-353A-1/c
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Best Local Similarity
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rei
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                           FEATURE
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                     240
                                               431 AGGTTCATTGTTGGAAGCGTTGGTGTAATCCACACCCTCTGTGCACGGGTTACAGGCTCC
                                                                                  180
                                                                                                        491 CATGGTGCAGGAACTTTTATGTTTTTGATCTGATTTACAAACTGTACATGGGAAGCAAGA 432
                                                                                                                                    120 CACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAA 179
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                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BROOKES, ANDERS REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/006,353A
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   CTTTGGCACACTTGAAGGGATGGTGATGGAGATGCCAATCCATGGAATCAG
                                                                             CCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTTCATTGTTGGAAGCGTTGGTGTAATCCACACCCTCTGTGCACGGGTTACAGGCTCC 310
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                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1392 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9410 KEY WEST AVENUE
                                                                                                                                                                  7.8%;
ilarity 48.3%;
Conservative
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RUBEN, STEVEN
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183..959
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261..959
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183..260
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                                                                                                                                                                                              DB 4;
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                                                                                                                                                                                              Length 1392;
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; LOCATION: (18:
US-09-573-986-1
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US-09-573-986-1/c
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Best Local Similarity
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SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/09/573,986
CURRENT FILING DATE: 2000-05-18
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                                                                                                                                                                                                                        TITLE OF INVENTION:
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ORGANISM: Homo
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                              ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth STREET: Suite 4700
                                          MEDIUM TYPE:
                                                                                           COUNTRY: U.S.A. ZIP: 90071-2066
             DPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTATGTTCTGATCTATGAGATCCTGCTGGACACTCCTCCCCCTTGAAGCTG
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Ruben, Steven
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                                                                                                                                                                                                                                                                                                                                          Fuller, Forrest H.
SYSTEM: IBM P.C. DOS 5.0 FastSEQ for Windows 2.0
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                           IBM Compatible
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48.3%;
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371 AGTATGTTCTGATCTATGAGATCCTGCTGGACACTCCTCCCCCTTGAAGCTG 320
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Tumor Necrosis Factor Receptor 5
DB 4;
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120 CACGGTTGTTAAGCCCCTGTTCTTTCCGTTGTTTAATCTTAATGTTCTTTGGAATAAAAA 179 Score 29.6; D Pred. No. 4.6; Mismatches ; 68 Length 1392; Indels 0 Gaps

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491 CATGGTGCAGGAACTTTTATGTTTTTGATCTGATTTACAAACTGTACATGGGAAGCAAGA 432 180 CCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGAC 239 CTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAATCAG 291 AGGTTCATTGTTGGAAGCGTTGGTGTAATCCACACCCTCTGTGCACGGGTTACAGGCTCC 372

Hammerland, Lance G.

"ENTION: CHIMERIC RECEPTORS AND METHODS TREATMENT OF NEUROLOGICAL METABOTROPIC GLUTAMATE RECEPTORS AND IDENTIFYING COMPOUNDS ACTIVE NEUROLOGICAL

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                                                                                                                                                               NAME/KEY: CDS
LOCATION: (117)..(1949)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: M24736/Genbank
DATABASE ENTRY DATE: 1994-11-07
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/209,668A CURRENT FILING DATE: 1998-12-10 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Monia, Brett P.

APPLICANT: Xu, Xiaoxing S.

TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ISPH-0336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 220/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                 LENGTH: 3834
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LENGTH: 4000 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/C
FILING DATE: July 26, 19
ATTORNEY/AGENT INFORMATION:
   3192
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                     114 AGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
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Local Similarity 50.7%;
hes 71; Conservative
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FILING DATE: July 25, 1996
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STRANDEDNESS: sing
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                                                                                        Local Similarity
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AAGATGTCTAATAGTTATTCCCTATTTGTTTTCTTCTGTATGTTAGGGTGCTCTGGAAGA 3251
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                                                                         78;
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Pred. No. 7
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Pred. No. 8
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US-08-365-470-1
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Best Local Similarity
                                                                                                                                                                                                          Matches
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                                                                                                                                    3192 AAGATGTCTAATAGTTATTCCCCTATTTGTTTTCTTCTGTATGTTAGGGTGCTCTGGAAGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08
FILING DATE: 05-AUG-1993
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MEDIUM TYPE: Floppy
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                                                                    3252 GAGGAATGCCTGTGTGAGCAAGCATTTATGTTTATTATAAGCAGATTTAACAATTCCAA 3311
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                      114 AGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Markowicz, Karen REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                              CENGTH:
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 AGGAATCTCCAGTTTTCAGTTGATCACTGGCAATGAAAA 3350
                          AGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGA 272
                                                                                                  TAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAA 233
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nilarity 49.1%;
Conservative
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 8.6;
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; Sequence 98, Ap
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                               3276 GAGGAATGCCTGTGTGAGCAAGCATTTATGTTTATTATAAGCAGATTTAACAATTCCAA 3335
                                                                                                                 3216 AAGATGTCTAATAGTTATTCCCTATTTGTTTTCTTCTGTATGTTAGGGTGCTCTGGAAGA 3275
                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
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APPLICATION DATA:

FILING PATER PCT/US91/05209
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ADDRESSEE: Woodland Falls Corporate Park
STREET: 210 Lake Drive East, Suite 201
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/567,286
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PRIOR APPLICATION DATA:
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234 AGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGA 272
                                                                                                                                                 114 AGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
                                                                                                                                                                              Local 5.
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                                                                                                                                                                                                                                                                                                TYPE: Nucleic Acid
STRANDEDNESS: Singl
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                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                   TAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAA 233
                                                                                                                                                                                                  Similarity
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ilarity 49.1%;
Conservative
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VENTION: Compositions and Methods for Preventing
VENTION: and Treating Allograft Rejection
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5883082ember 23,
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                                                                                                                                                                                Score 29.4; DB Pred. No. 8.6; 0; Mismatches
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US-09-009-490A-88
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GENERAL INFORMATION:
                                                                                                                                        Matches
                                                                                                                                                                      Query Match
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3276 GAGGAATGCCTGTGTGAGCAAGCATTTATGTTTATTATAAGCAGATTTAACAATTCCAA 3335
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: August 14, 1
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: MAY 12, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 063,167
FILING DATE: MAY 17, 1993
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                                                                     3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 939,855
FILING DATE: September 2, 1:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: DISKETT
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                                       174
                                                                                        114 AGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 969,151
FILING DATE: February 10, 1993
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                                                                                                                                     Local Similarity 49.1
es 78; Conservative
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                                                               AAGATGTCTAATAGTTATTCCCTATTTGTTTTCTTCTGTATGTTAGGGTGCTCTGGAAGA 3275
                               TAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAA 233
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VENTION: Oligonucleotide Modulation
VENTION: of Cell Adhesion
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49.1%;
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234 AGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGA 272

AGGAATCTCCAGTTTTCAGTTGATCACTGGCAATGAAAA 3374

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RESULT 15
US-08-482-073-1
  Query Match 7.8%;
Best Local Similarity 49.1%;
Matches 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE: 31-OCT-1990

PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO PCT/US 90/02357

PILING DATE: 27-APR-1990

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/452675

PILING DATE: 18-DEC-1989

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/359516

PILING DATE: 01-JUN-1989

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/354151

APPLICATION DATA:
                                                                                                                                                                                             TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B124CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                              SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 3863 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,073
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,336
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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                                                                                                                      STRANDEDNESS:
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1251 Avenue of the Americas
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ROSA, Margaret D.
VENTION: ENDOTHELIAL CELL-LEUKOCYTE ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hession, Catherine A.
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28-APR-1989
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  Score 29.4; D
Pred. No. 8.6;
0; Mismatches
                                    DB 4; Length 3863;
    81;
  Indels
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Gaps
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Search completed: January 31, 2003, 01:14:56 Job time: 88 secs

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Title:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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378
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AUTHORS
TITLE
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BM987874/c
LOCUS
DEFINITION
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KEYWORDS
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BG136484	AZ534719	BJ068145	AW635726	AA711119	AI651773	BE067501	AZ182824	BQ024523	AW444676	AZ083843	AW190856	AQ419832	AI828325	BB481722	AW231608	CNS044QP	AZ400532	AV413421	BI861604	AZ182814	BB566524	BM973205	AZ720218	AI781854	CNS00AMP	AW704405	A1600177	0894	775	9346	AZ191123	AZ108808	AQ922388	AL628007	вQ392762		вн853295	BQ655384
BG136484 EST477022	AZ534719 ENTBW93TR	.BJ068145 BJ068145	b137d10	AA711119 vt56b05.r	b501	MR4	8P_019	Ħ.	UI-H-B]	RPCI-2:	x142f09	AO419832 RPCI-11-1	k83d06.	BB481722 BB481722	AW231608 687067H09	AL274426 Tetraodon	AZ400532 1M0166D23	AV413421 AV413421	BI861604 603390466	AZ182814 SP_0190_A	BB566524 BB566524	BM973205 UI-CF-EC1	AZ720218 RPCI-24-1	AI781854 EST262733	AL055267 Drosophil	sk30f07.	AI600177 EST251880	t13d12.x	A0775948 HS 2151 B	±07d11.x	SP 1018	RPCI-23	RPCI-23-	L628007	NISC mg2	60317	SALK 076	NXRV093

ALIGNMENTS

source human.

human

human

human

flow sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 451)

RS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

AL Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov UI-H-COO-asz-a-11-0-UI.sl NCI_CGAP_Sub9 Homo sapiens cDNA clone IMAGE:5860149 3', mRNA sequence. Seq primer: Ml3 FORWARD POLYA=Yes. BM987874.1 GI:19707263 Location/Qualifiers 1. .451 EST 17-JUN-2002

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
AI459918/c
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Best Local
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                              Washington University School of Medicine 4444 Forest park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                             White,Y., Wylle,T., WaterstowashU-NCI human EST Project Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                           Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Materston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI459918
439 bp
ar81h09.x1 Barstead colon HPLRB7
IMAGE:2151713 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 439)
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est@watson.wustl.edu
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/clone_lib="NCI_CGAP_Sub9"
/tissue_type="mixed"
/dev_stage="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      information, contact: Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.4%;
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RESULT 3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120;
                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Insert Length: 508 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 234.
Location/Qualiflers
                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 386)
                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                                                                                                                mRNA sequence.
AA743908
                                                                                                                                                                                                                                                                                                                                                        AA743908 386 bp mRNA linear EST 19-FEB-199
ob05b10.sl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322779 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                   AA743908.1 GI:2784658
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/clone="IMAGE:1322779"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2151713"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Barstead colon HPLRB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

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REFERENCE
AUTHORS
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BG197212/c
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262 GGTGATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGCAG 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 ATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGCAGAAGT 325
                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               806 bp mRNA linear EST 21-APR-2001
RST16451 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG197212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 806)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: scain@athersys.com
                                                                                                 Similarity
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                                                                                                                                                                             /note="See 'Creation of Genome-wide Protein Expression' Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

a 187 c 155 g 205 t 7 others
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                                                                                                                                                                                                                                                                                                                                                /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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77 c 73 g
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98.2%;
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                                                                   Score 79.4; DB 12;
Pred. No. 2.6e-12;
0; Mismatches 1;
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Best Local (
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                                                                                                                                                                                       146 CCGTTGTTT 154
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                                                                                                                                                          91
                                                                                                                                                                                                                                     86 CAAGCTTGAATGTGTGTTCTGGAGGTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTT 145
                                                                                                                                                                                                                      31 CAAGCTTGAATGTGTGTTCTGGAGCTGAAGGATGTACGGTTGTTAAGCCCCCTGTTCTTTT
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sequence.
AQ035738
AQ035738.1
GSS.
                                                               CIT-HSP-2321C21.TF CIT-HSP
                                                                                                                                                                                                                                                                                  65; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Building (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2319N3.TR
                                                                            AQ035738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams, M.D., Rounsley, S.D., Zhao, Solden, K., Berry, K., Granger, D., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 bp DNA linear GSS 11-JUL-1998 CIT-HSP-2319N3.TF CIT-HSP Homo sapiens genomic clone 2319N3, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
Clines are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a random BAC End Sequence Database for Sequence-Ready Map
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                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                             85
                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1:
HindII"
                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="2319N3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="CIT-HSP"
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                                                                                                                                                                                                                                                                                               Score 62.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                          84 g
                                                                          237
                                                                                                                                                                                                                                                                                  Mismatches
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                                                             Homo
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                                                        DNA linear GS sapiens genomic clone
                                                                                                                                                                                                                                                                                            1.7e-07;
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                                                                                                                                                                                                                                                                                                            DB 17;
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Matches 42
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                                                                                                                        Unpublished (2000)
Contact: Johnson, Arthur
Conthact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                          Pinus taeda
Eukaryota; Viridiplantae;
Spermatophyta; Coniferopsi
                                                                                                                                                                                                                                                                                                                                                                   B0655384 554 bp m
NXRV093_F11_F NXRV (Nsf Xylem Root w
clone NXRV093_F11 5', mRNA sequence.
                                                                                                      Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                            Sederoff, R.
                                                                                                                                                                                                                                                                                                                                            BQ655384
BQ655384.1 GI:21787710
                                                                                                                                                                                                         Molecular Basis of Wood Formation
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
Clones are available from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_GSSs: CIT-HSP-2321C21.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a random BAC End Sequence Database for Sequence-Ready Map Bullding (1998)
                                                                                                                                                                                                                                                                                                            oblolly pine.
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Homo sapiens
                                                                                          primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%;
nilarity 97.7%;
Conservative
/organism="pinus taeda"
/strain="Coastal plain loblolly pine
/db_xref="taxon:3352"
                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                     idiplantae; Streptophyta; Embryophyta; Coniferopsida; Coniferales; Pinaceae;
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(ylem Root wood
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               North Carolina"
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Pinus; Pinus.
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taeda cDNA
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                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 TTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAA 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGGTGGCGCAGCTATGTTGGTAGCTATAGCAGA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTG 227
                                                                                                                                                                                                                                                                                      Arabidopsis Genome
(7001)
(Onpublished (2001)
(Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
(10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                     This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (Dases 1 to 439)
1 (Dases 1 to 439)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
Alonso,J.M., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH853295 439 bp DNA linear GSS SALK_076311.54.00.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK_076311.54.00.x,
                                                                                                                                                                                      Class: TDNA tagged.
                                                                                                                                                                                                              At2g41810
                                                                                                                                                                                                                                                                     Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,C., Jeske,A., Karnes,M., Kim,Č.J., Parker,H., Prednis,L
, Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
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BH853295
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/db.xref="taxon:3702"
/db.xref="taxon:3702"
/clone="SALK_076311.54.00.x"
/clone_lib="Arabidopsis thallana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thallana lines
                                                                                               /strain="Columbia
                                                                                                                     /organism="Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="XL1-Blue"
//note="Vector: pBlueScript SK-; Site_1: Eco RI; Site_2:
XhoI; The library is from primary xylem scraped from the
roots of a twelve year old tree in the transitional phase
from juvenile wood to mature wood production. NOTE: The
sequences contain a 'cDNA adapter' between the EcoRI site
and the start of the EST. The adaptersequence is
'AATTCGGCACGAG'."

88 c 131 g 161 t 21 others
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="NXRV093_F11"
/clone_lib="NXRV (Nsf Xylem Root wood Vertical)"
/tissue_type="Xylem"
/cell_type="Root (primary)"
/dev_stage="Transitional"
                                                                                                                                               . 439
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Best Local S
Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                      Plate: LLAM11638 row: 1 column: High quality sequence stop: 102. Location/Qualifiers 1. 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999 Contact: Robert S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
1 (bases 1 to 1237)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal: Site_2: NotI; Cloned unidirectionally. Primer: Oligo di Library constructed by Life Technologies. Investigators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" a 68 c 68 g 146 t 2 others
                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:5252883"
                                                                                                                       providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                            /clone_11b="NCI_CGAP_Mam5"
/tlssue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
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                  10.3%;
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53.2%;
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IMAGE:5252883 5',
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JOURNAL COMMENT
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SOURCE
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Best Local
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                                                                            144 TTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGT 203
204 TTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACACTTGAAGGGATGG
                                                       405 TIGCCATGGAGACTCTGATTTCCTTGGGATTTGAAAGGGTTCTTACTAGTGGCTGTGACA 464
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83; Conser
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
cDNA Sequencing by: National Institutes of Health Intramural
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Seq primer: M13RP1 reverse primer
Location/Qualifiers
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NISC_mq26d04.yl NICHD XGC Emb5 S

IMAGE:5384863 5', mRNA sequence.

BQ392762

BQ392762.1 GI:21080449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    info@image.llnl.gov
Plate: LLAM11980 ro
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Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
National Institute of Child Health and Human Development, National
Cancer Institte, Xenopus Gene Collection
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                                                                                                                                                                                                                /clone_lib="NICHD XGC Emb5"
/tissue_type="gastrula"
/dev_stage="embryo, stages 10-13"
/lab_host="DHLOB (phage-resistant)"
/note="Vector: pCMV-SPORT6.ccdb; Site_1: Not1; Site_2: ECORV; Cloned unidirectionally. Primer: Oligo dT. Avera insert size 2.0 %b. Constructed by Invitrogen. Note: This a Xenopus Gene Collection (XGC) library."

109 c 163 g 172 t
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="IMAGE:5384863"
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                                                                                                                                                 10.1%;
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                                                                                                                                                 Score 38; DB 14; Pred. No. 2.6;
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                                                                                                                                                                        TCATAGTAATGCCAGGTGGCGGCATTACTGAGCGAAAC 606
                                                                                                                                                                                                                                     CGTCTGCTTTGGAAGGTTTGCCTTTAATAAAGAGACTTGTGGAACAAGCCAAAGGACGAA 568
                                                                                                                                                                                                                                                                                                       TGATGGAGATGCCATCCATGGAATCAGGTGGCGCAGC 301
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                                                                    RPCI-23-27685.TJ RPCI-23
                 AQ922388
AQ922388.1 GI:6611391
                                                     DNA sequence.
                                                                                           AQ922388
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas022e21.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001) Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sanger Centre
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Silurana tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="garrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XLI-blue"
/note="Vector: pCS107; Site_1: EcoRI, Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
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/clone_lib="XGC-gastrula"
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/db_xref="taxon:8364"
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Pred. No.
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                                                           Mus musculus genomic clone RPCI-23-276B5,
                                                                                    592 bp
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                                                                                                                                                                                                                                                                                                                                      DNA sequence.
AZ108808
                            RPCI-23-25N18.TV RPCI-23
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Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 276 row: B column: 5
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                               580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Sha, Levins, M., Mcgann, S., Tsegaye, G., Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,B., Levins,M., and Fraser,C.M.
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/clone="RPCI-23-276B5"
/clone_lib="RPCI-23"
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/strain="C57BL/6J"
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Pred. No. 3.9;
0; Mismatches
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                       Mus musculus genomic clone
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GSS 09-MAY-2000 RPCI-23-25N18,

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REFERENCE
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AZ191123

B29 bp DNA linear GSS 30-AUG-2000 SP_1018_B2_D06_T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1018 Col-12 Row-H, DNA sequence.

AZ191123

AZ191123.1 GI:8374302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: szhao@tlgr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 25 row: N column: 18
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Fax: 301 838 0208
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Other_GSSs: RPCI-23-25N18.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: T7
Class: BAC ends.
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
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Mammalia; Eutheria; Rodentia;
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1 (bases 1 to 699)
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/clone="RPCI-23-25N18"
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Sciurognathi; Muridae;
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5.3;
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                                                                                                                                                                                                                                                                                                                                                                                                   271 GATGCCAATCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                     Mus musculus
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 473)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoldea; Echinacea; Echinoida;
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cameron, RA, Davidson, EH
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                  AI449346
mt07d11.x1 Soares mouse
3', mRNA sequence.
AI449346
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Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 1018 row: H column:
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Class: BAC ends
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Location/Qualifiers
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DH108"
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/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
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/db_xref="taxon:7668"
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Rodentia;
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Pred. No. 5.5;
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Best Local Similarity 54.4%;
Matches 74; Conservative
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                                                                241 TTTGGCACACATTGAA 256
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168 TTGGGCCTACATTGAA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 402.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M.WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                143 a
                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:620373"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen
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ALIGNMENTS

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XX HO Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss 09-MAR-2001; 2001WO-US07787. 13-SEP-2001. WO200166753-A2 Homo sapiens Novel human diagnostic and therapeutic gene #222 17-DEC-2001 AAS37164; AAS37164 standard; cDNA; 378 BP (first entry)

WPI; 2001-530177/58 Williams LT, Escobedo J, Innis MA, Gar Reinhard C, Randazzo F, Kennedy GC, Po Drmanac R, Crkvenjakov R, Dickson M, I Leshkowitz D, Kita D, Garcia V, Jones Garcia PD, Sudduth-Klinger
Pot D, Kassam A, Lamson G
, Drmanac S, Labat I;
nes WL, Stache-Crain B;

09-MAR-2000; 2000US-0188609

(CHIR) CHIRON CORP. (HYSE-) HYSEQ INC.

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Matches 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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      13-SEP-2001.
                        WO200166753-A2
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RESULT 3
AAS37237
ID AAS3
XX
AC AAS3
XX
DT 17-D
XX
DE NOVE
XX
VX
KW Huma
XX
VX
PD HOMO
XX
PD 13-S
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39338 represent novel human diagnostic and therapeutic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides and polypeptides, useful treatment of breast, lung and colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac R, C:
Leshkowitz D,
                                                                                                                              Novel
                                                                                                                                                       17-DEC-2001
                                                                                                                                                                                      AAS37237;
                                                                                                                                                                                                              AAS37237 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                    321
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                                                                    sapiens
                                                                                                                                                                                                                                                                                   TCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATGACGCAGCGGCTCTTAGAGGAACATATGGAAAACACCCCAAGCCGGAGTCTCTCACA
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                                                                                                                                                                                                                                                                                                              TCTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATGACGCAGCAGCTCTGAGAGGAACATAAGGAAAACACCCCAAGCCGGAGTCTCTCACA
                                                                                                                            human
                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 BP; 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Randazzo F, Kennedy GC, Po
Crkvenjakov R, Dickson M, I
D, Kita D, Garcia V, Jones
                                                                                                                            diagnostic
                                                                                                                                                                                                                                                                                                              333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INC.
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                                                                                                  breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1193pp;
                                                                                                                                                                                                               CDNA;
                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 64 C;
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                                                                                                                            and
                                                                                                lung;
                                                                                                                            therapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 299.6; DB 22;
Pred. No. 6.8e-87;
0; Mismatches 4;
                                                                                                 colon;
                                                                                                                                                                                                               ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 G;
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2, €.
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                                                                                                 prostate;
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, Pot D, Kassam A,
M, Drmanac S, Labat
Ones WL, Stache-Crai
                                                                                                                            gene
                                                                                                                              #295
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Stache-Crain
                                                                                                 cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                 diagnostic;
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Sudduth-Klinger Labat I; 8

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RESULT 4
AAS37242
ID AAS3
XX AAS3
AC AAS3
XY 17-E
XX NOV6
XX HUMB
XX HOMC
XX H
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Best Local
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                                                                                                                                                              Novel human diagnostic and therapeutic gene #300
                                                      WO200166753-A2
                                                                                               Homo
                                                                                                                                                                                                               17-DEC-2001
                                                                                                                                                                                                                                                     AAS37242;
                                                                                                                                                                                                                                                                                      AAS37242 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams LT, Escobedo J, Innis MA, (Reinhard C, Randazzo F, Kennedy GC, Drmanac R, Crkvenjakov R, Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-2000; 2000US-0188609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides and polypeptides, useful atment of breast, lung and colon cancer -
                                                                                                                                                                                                                                                                                                                                                                           GGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATGACGCAGCGGCTCTTAGAGGAACATATGGAAAACACCCAAGCCGGAGTCTCTCACA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-530177/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282;
                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 BP; 90 A; 64 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 670; 1193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention.
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                                                                                                                             breast;
                                                                                                                                                                                                                                                                                        CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%;
98.6%;
                                                                                                                         lung; colon; prostate; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 279.6;
Pred. No. 2e-8
0; Mismatches
                                                                                                                                                                                                                                                                                      ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garcia PD, Sudduth-Klinger
Pot D, Kassam A, Lamson
, Drmanac S, Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2e-80;
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Stache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                                                                                                                                                                   313
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RESULT 5
ABL33878
ID 3818
ID 3818
IX ABL3
AC ABL3
XX DT 26-M
XX DT 26-M
XX Huma
XX Huma
XX Huma
KW anti
KW neur
KW neur
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        Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; anti-HIV; cancer; eye disease; arteriosclerosis; anaemia; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to new polynucleotides and polypeptides, useful fo diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39338 represent novel human diagnostic and therapeutic coding
                                                                                                                                                                                                                   ABL33878
                                                                                                                                                                                                                                                   ABL33878 standard; DNA; 5378
                                                                                                                                                                            26-MAR-2002
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Reinhard C, Randazzo F, Kenne
Drmanac R, Crkvenjakov R, Dic
Leshkowitz D, Kita D, Garcia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences
                                                                                                                                                                                                                                                                                                                                                      276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides, useful treatment of breast, lung and colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                         268
                                                                                                                                                                                                                                                                                                                                                                                                                                216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                   GGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA
                                                                                                                                                                                                                                                                                                                                              GGAGATGCCAATCCATGGAATCAAGTGGCACAGCTATGTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACACTTGAAGGGATGGTGAT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATGACGCAGCAGCTCTGAGAGGAACATAAGGAAAACACCCAAGCCGGAGTCTCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTTGAATGTGTTCTTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCC
                                                                                                                                   immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278;
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                                                                                                                                                                      entry)
                                                                                                                             associated gene SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innis MA,
Kennedy GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 275; DB 22;
Pred. No. 6.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ζ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones
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Pot D, Ka
, Drmanac S
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Stache-Crain
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RESULT 6
ABA08523
ID ABA0
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AC ABA0
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DT 11-J
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Best Local :
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           inhibin; chemo proliferation;
                                                                        Human
                                                                                                                                                                                                                                                                                                                                               1377
                 Human; cytokine; cell proliferation; cell differentiation; grahamatopolesis regulation; tissue growth; immunomodulator; acinhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
                                                                                              11-JAN-2002
                                                                                                                                                                                                     1557
                                                                                                                                                                                                                                                    1497
                                                                                                                                                                                                                                                                                                1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                      ABA08523;
                                                                                                                                            ABA08523 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modifor diagnosis and treatment of diseases associated cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5378 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases. The present sequence is a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                          317
                                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                       137
                                                                                                                                                                                                                                                                                                            ACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAA
                                                                                                                                                                                                                                                                                                                                                         TGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGT
                                                                                                                                                                                                                                                              GGGATGGTGATGGCAATGCCAATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTAT
                                                                                                                                                                                                                                                                                             ACGAAGTTTAGTGATTTATTTCGGATCGTTGTTGAGAATGGAGGTTTTTTAAATATTAAG
                                                                                                                                                                                                                                                                                                                                             AATTGAGTAATTATTAG
                                                                                                                                                                                                                         AGCAGAAGTCTTCTTGG
                                                                        secreted
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention provides
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2000DE-1043826
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                                                                       protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1499
                                                                                                                                          CDNA; 492
                                                                                                                                                                                                                                                                                                                                                                                                       48.2%;
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                                                                      homologue-encoding
                                                                                                                                                                                                                          333
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 134 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32pp +
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                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.1
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.8;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                         1201 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemically modified ases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                         2544 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the
                                                                      CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                           102;
                                                                      SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                      0 other;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5378;
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                                                                      NO:299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene, useful
abnormal
                              activin;
                                           growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                         factor;
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CC haematopoiesis regulatory activity; tissue growth activity;

CC haematopoiesis regulatory activity; tissue growth activity;

CC chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC the invention are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders); chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,

CC polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC manipulate and fungal infections in addition to immune disorders.

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC manipulate and fungal infections in addition to immune disorders and nucleotides

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC manipulate and fungal infections in addition to immune disorders.

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC manipulate and fungal infections in addition to immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasctropic; cardiant; virucide; antibac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 440; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000;
27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-2001; 2001WO-US03800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human proteins and DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ofeins and DNA encoding sequences useful for preventing, or ameliorating a medical condition in a mammalian subject
                                                                       techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                           polypeptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulnerary; antiulcer; ss.
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2000US-0560875
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                                                                present sequence represents
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Sequence

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RESULT 7
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                       The present sequence is one of a large number of 5' ESTs derived from C mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from C total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) C of the mRNA because they are often obtained from oligo-dT primed cDNA ilbraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer C DNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design cerview.
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                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
 Sequence
                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 33882; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein 5' EST, SEQ ID NO: 33882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC29807 standard; cDNA; 158 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 TTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTT 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAACATGCTTTGACT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATATAATGTGCTGATTTTAACAATGCAGGCCTCACTGCCAAAAGTTCTTCGGTTTTGTGC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAACCTCTACGCTCTTGGTTTGGGTTGGAGTCATCAGATACCTGGGTTATTTCCAGGC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 8.9%;
Similarity 52.9%;
   158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
 B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9905-0122487
35
A; 34 C;
                                                                                                                                                                                                                                                                                                                                                                                                       Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
34 G; 55 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33.6; D
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Query Match Best Local Similarity Matches 70; Conserv

53.48;

Score 33.4; Pred. No. 0.

0.9;

DB 21; 61;

Length 158; Indels

0

Gaps

0

RESULT 9
AAZ24100/c
ID AAZ241
XX

AAZ24100 standard;

DNA;

240

밁 QY

60

148 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTT 206

GTGGGACAATCTGATGCTATATCTAAGAAAAACCTCCGTGCCAAGTCGAAGTTGCTTTT 2

Matches Query Match Best Local :

Local Similarity

8.8%;

Score 33.4; DB Pred. No. 1.1; 0; Mismatches

DB 20; 16;

Conservative

0;

Indels

0

0

Mismatches

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RESULT 8
AAZ24099/c
ID AAZ240
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                       This invention describes a novel method for determining the absolute mutagenicity of a substance. The method is used to determine the mutation rate associated with particular substances and the error rates for polymerases during amplification reactions. It is therefore useful for monitoring nutrients or medicines and environmental factors such as radiation from televisions or computer screens. The method is applicable to all types of mutations (collectively or individually), is unaffected by repair mechanisms or in vivo selection mechanisms, and is an in vitro process so animal testing is not required. AAZ24098-Z24105 represent rat NF-1 DNA fragments used to illustrate the method of the invention.
Sequence 240 BP; 66 A; 53 C; 53 G; 68 T; 0 other;
                                                                                                                                                                                                                         Method for determining absolute mutagenicity and error rate polymerases in amplification reactions \, -
                                                                                                                                                                                               Examples; Fig 5; 18pp; German.
                                                                                                                                                                                                                                                                        WPI; 1999-602407/52
                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
                                                                                                                                                                                                                                                                                                                                  (HARJ/) HARJES
                                                                                                                                                                                                                                                                                                                                                                24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE19818422-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NF-1; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat NF-1 DNA fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ24099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ24099 standard; DNA; 240 BP
                                                                                                                                                                                                                                                                                                                                                                                                                          28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   radiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGGTTGTTAA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAACACCCAAGCCGGAGTCTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGATGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATAGCTCCTGAGGAGGCCACAAAGGGAAATCTCCATTCATCTCTTCCTGCTACAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACGGCTGCTTAAGACGACTTAAGGGGGAATGACGCAGCGGCTCTTAGAGGAACATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer; mutagenicity; mutation rate; polymerase error rate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                98DE-1018422
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Best Local S
Matches 43
08-OCT-1999;
                                                  WO200022430-A2
                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification;
                                                                                                                                                      N. meningitidis partial DNA sequence
                                                                                                                                                                                04-DEC-2000
                                                                                                                                                                                                                                 .467/c
AAA81467 standard; DNA; 25509 BP
                                                                                                                                                                                                                                                                                                                                                                                                                          for monitoring nutrients or medicines and environmental factors such as radiation from televisions or computer screens. The method is applicable to all types of mutations (collectively or individually), is unaffected by repair mechanisms or in vivo selection mechanisms, and is an in vitro process so animal testing is not required. AA224098-Z24105 represent rat NF-1 DNA fragments used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for determining the absolute mutagenicity of a substance. The method is used to determine the mutation rate associated with particular substances and the error rates for polymerases during amplification reactions. It is therefore useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for determining absolute mutagenicity and polymerases in amplification reactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NF-1; rat; radiation;
                         20-APR-2000
                                                                              Neisseria
                                                                                                  antigen; vaccine; diagnosis;
Meningococcus B; MenB; ds.
                                                                                                                                                                                                           AAA81467;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 240 BP; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examples; Fig 5; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-602407/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harjes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARJ/) HARJES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat NF-1 DNA fragment 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000
                                                                                                                                                                                                                                                                                                                        148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ24100;
                                                                                                                                                                                                                                                                                               60 GTGGGACAATCTGATGCTATATCTAAGAAAAACCTCCGTGCCAAGTCGAAGTTGCTTTT 2
                                                                                                                                                                                                                                                                                                            GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTT 206
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                             meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer; mutagenicity; mutation
ss.
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
99WO-US23573.
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                                                                                                                                                                                                                                                                                                                                                                                                     A; 53 C;
                                                                                                                                                                                                                                                                                                                                                             8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                Score 33.4; Di
Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 0:
                                                                                                                                                                                                                                                                                                                                                                                                    53 G;
                                                                                                                                                                                                                                                                                                                                                                                                 68 T; 0 other;
                                                                                                                                                    gnm_15
                                                                                                                                                                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rate; polymerase error rate;
                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          error rate
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                          Length 240;
                                                                                                                                                       NO:15
                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                0
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RESULT 11 AAF21607/

AAF21607

standard; DNA;

349980 BP

맑 ğ В

23185

289

CAGGTGGCGCAGCTATGTT

307

TAATTGGAGCAGCTATATT 23167

X B X B X B X B X B

13-MAR-2001

(first entry)

Neisseria meningitidis B nucleotide sequence

SEQ ID

NO:108

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229

TGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAAT

23305 TGATATAAAAATCATCCAAGAAAACATTAATAATTTTTGGAATAATTGTCCCTTTAATAT 23246

169 TGGAATAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGT 228

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Query Match Best Local S Matches 73

Similarity

8.8%; nilarity 52.5%; Conservative

0;

Score 33.4; D Pred. No. 8.4; O; Mismatches

8.4; В

Length 25509; Indels

66; 21;

0

Gaps

0

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CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC represent specifically claimed Neisseria meningitidis genomic DNA
CC sequences; AAA81260 to AAA81303 and AAB2560 to AAB25663 represent
CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC AAA81259 and AAA81304 to AAA81321 represent pCR primers used in the
CC AAA81452 represent Neisseria meningitidis DNA sequences; and AAA81332 to
CC AAA81452 represent Neisseria meningitidis DNA sequences; and AAA81322 to
CC AAA81452 represent Neisseria meningitidis Man polynucleotide ORF
CC sequences, which are all used in the examplification of the present
CC invention. The nucleic acid sequences, protein sequences, and antibodies
CC against them, can be used in the manufacture of a composition. The
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC exposed proteins all pathogenic Neissariae. Identification of sequences
CC and/or against all pathogenic Neissariae. Identification of sequences
CC particularly organism-specific probes. Attempts to make efficacious
CC Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC Multivalent vaccines have also been tried but none have successfully
CC exposed proteins that may be presumed targets for the immune system and
CC which are not antigenically variable or at least more conserved than
CC other more variable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frazer CM, H
Masignani V,
       Sequence 25509 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 399-406; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other Neisserial infections, for example, N.gonorrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleotide sequences of Neisseria meningitidis used in the diagnosis and treatment of N. meningitidis \boldsymbol{\theta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-1998;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP.
                                                                           variable regions.
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Galeotti
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99US-0132068
6157 A; 6156 C; 6549 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peterson
C, Mora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,
Ά (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tettelin H, Venter
Ratti G, Scarselli
   6647
   H.
0 other;
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CC Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 CC to AAF21613 represent fragments of the NMB genomic sequence, as the CC sequence was too long to go in a record on its own it was split into 8 cs sequences which overlap each other at the beginning and end of each CC sequences which overlap each other at the beginning and end of each CC sequences which overlap each other at the beginning and end of each CC the beginning of AAF21608, and so on). AAF21544 is repeated at CC the beginning of AAF21608, and so on). AAF21545 to AAF21587 are repeated at CC each color of CC CAAF21606 represent PCR primers which are used in the exemplification of CC CAAF21606 represent PCR primers which are used in the exemplification of CC each color of CC CAAF21606 represent of CC can be used in vaccines and gene therapy. CC existerial activity, and can be used in vaccines and gene therapy. CC existerial activity, and can be used in vaccines and gene therapy. CC existerial activity and can be used in vaccines which binds to the CC existerial bacteria or as a diagnostic reagent for detection the to Neisserial bacteria or as a diagnostic reagent for detecting the CC concing sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are used for the opportunities to find antigenic or immunogenic proteins which are used in vaccines than the outer membrane proteins which are used for the other in vaccines than the outer membrane proteins which are used.
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Best Local
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Galeotti C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-1999; 99US-0132068
08-OCT-1999; 99WO-US23573
28-FEB-2000; 2000GB-0004695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-647603/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2000; 2000WO-US05928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Appendix A; 692pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis B full length frames are used to detect, treat and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frazer CM, Grand1 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                      Sequence 349980 BP; 84410 A; 84863 C; 94187
                                                                                                                                                                                           169
                                                                                                                                                                                                                                                  Local Similarity
                     CAGGTGGCGCAGCTATGTT 307
                                                                                                                                                   TGATATAAAAATCATCCAAGAAAACATTAATAATTTTTTGGAATAATTGTCCCTTTAATAT 75809
                                                                                                                                                                                       TGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGT 228
                                                                         TGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAAT 288
TAATTGGAGCAGCTATATT 75730
                                                                                                                                                                                                                            73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hickey E,
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mora M,
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99WO-US23573.
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, Ratti G, Scarselli M,
                                                                                                                                                                                                                                8.8%; Score 33.4; I
52.5%; Pred. No. 27;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome sequence and open reading prevent Neisserial infections -
                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                              G; 86520 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scarlato V,
                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                      Length 349980;
                                                                                                                                                                                                                                    Indels
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Rappuoli R;
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                    0,
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2729

AXX57669/c
XX
AXX57669;
XX
AXX57669;
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AXX57669;
XX
O6-NOV-2001 (first entry)
DT
O6-NOV-2001 (first en

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14-SEP 2000
21-SEP 2000
21-SEP 2000
25-SEP 2000
25-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
20-OCT 2000
20-OCT
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2000US-0234998
2000US-02354814
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2000US-0235834
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2000US-0236369
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2000US-0246521
2000US-0249211
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RESULT 13
AAZ24101/c
ID AAZ241
XX
AC AAZ241
XC AAZ241
XX
DT 04-FEB
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK5442 to AAK5450 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 90
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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
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P-PSDB;
                      04-FEB-2000
                                                             AAZ24101;
                                                                                                       AAZ24101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 303 BP; 100 A; 62 C; 45 G; 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
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                                                                                                                                                                                                                                                                                                                                                            CTCTCTCACACATGATTTCATGTGCTCTGCCCCAATCCTGTAAAGTATTATAGCTCTCCT
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DB; AAM84888.
                                                                                                                                                                                                     GGTCTTT
                                                                                                                                                                                                                                            TGGTTTT
                                                                                                                                                                                                                                                                                                                       TCTTTTCCGTTGTTTAATCTAATGTTCTTTTGGAATAAAAACCTCCCTGCCAAGTAGTACT
                                                                                                                                                                                                                                                                                                                                                                                  CTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGGGTGGGGAGGCTGCCCAAGTCAGAAATGGCAATTAAGAAAAACAAATGTACAGAACC
                                                                                                                                                                                                                                                                                     TGTTTCTCAGGGGTTCGGTGAATGCTGCTTTTAAGGTTAACATGAATAGACAAWAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2729; 3071pp + Sequence Listing; English
                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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2000US-025179
2000US-0251479
2000US-0251856
2000US-0251868
2000US-0251869
2000US-0251989
2000US-0251989
2000US-0251990
2000US-0251997
2000US-0254097
2001US-0259678
                  (first entry)
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                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%;
48.1%;
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                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 2
Pred. No. 1.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM;
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T; 2 other; 22; 96;

Length 303 Indels

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Gaps

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199

139 238

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RESULT 14
ANZZ4102/c
ID ANZZ41
XX AZZ41
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel method for determining the absolute mutagenicity of a substance. The method is used to determine the mutation rate associated with particular substances and the error rates for polymerases during amplification reactions. It is therefore useful for monitoring nutrients or medicines and environmental factors such as radiation from televisions or computer screens. The method is applicable to all types of mutations (collectively or individually), is unaffected by repair mechanisms or in vivo selection mechanisms, and is an in vitro process so animal testing is not reguired. AAZ4098-Z24105 represent rat NF-1 DNA fragments used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NF-1; rat; radiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE19818422-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for determining absolute mutagenicity and polymerases in amplification reactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-602407/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARJ/) HARJES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ24102 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Examples; F1g 5; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat NF-1 DNA fragment 4.
                                                                                                                                                                                                                                   DE19818422-A1
                                                                                                                                                                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                                                                                                      radiation;
                                                                                                                                                                                                                                                                                                                                                           NF-1; rat;
                                                                                                                                                                                                                                                                                                                                                                                                              Rat NF-1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ24102;
                                                                                                                                                                                28-OCT-1999.
                          (HARJ/) HARJES
                                                                             24-APR-1998;
                                                                                                                             24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 AATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 AATCTGATGCTATATCTAAGAAAAACCTCCGTGCCAAGTCGAAGTTGCTTTT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 40; Conserv
                                                                                                                                                                                                                                                                                                                                      primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer; mutagenicity; mutation rate; polymerase {\tt ss}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B₽;
                                                                                                                                                                                                                                                                                                                                                                                                            fragment 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                98DE-1018422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 240
                                                                                                                                                                                                                                                                                                                                                              mutagenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
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                                                                                                                                                                                                                                                                                                                                                              mutation rate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                              polymerase
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                                                                                                                                                                                                                                                                                                                                                                 error rate,
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   to all typ
            This invention describes a novel method for determining the absolute mutagenicity of a substance. The method is used to determine the mutation rate associated with particular substances and the error rates for polymerases during amplification reactions. It is therefore useful for monitoring nutrients or medicines and environmental factors such as radiation from televisions or computer screens. The method is applicable to all types of mutations (collectively or individually), is unaffected
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NF-1;\ rat;\ primer;\ mutagenicity;\ mutation\ rate;\ polymerase\ error\ rate;\ radiation;\ ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ24103 standard;
                                                                                                                                                           Method for determining absolute mutagenicity polymerases in amplification reactions -
                                                                                                                                                                                                       WPI; 1999-602407/52.
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                                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat NF-1 DNA fragment 6
                                                                                                                               Examples;
                                                                                                                                                                                                                                   Harjes
                                                                                                                                                                                                                                                              (HARJ/) HARJES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 AATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTT 206
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nes 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATCTGATGCTATATCTAAGAAAAACCTCCGTGCCAAGTCGAAGTTGCTTTT
                                                                                                                                F1g 5; 18pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                           98DE-1018422
                                                                                                                                                                                                                                                                                                                       98DE-1018422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 240 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
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                                                                                                                                                                              error
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                                                                                                                                                                              rate
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mechanisms

or in vivo selection

mechanisms, and

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CC process so animal testing is not required. AAZ24098-Z24105 represent CC rat NF-1 DNA fragments used to illustrate the method of the invention. XX SO Sequence 240 BP; 66 A; 52 C; 54 G; 68 T; 0 other; Source 32 B; DB 20; Length 240; Best Local Similarity 76.9%; Pred. No. 1.7; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Sourch completed: January 31, 2003, 01:17:24

Search completed: January 31, 2003, 01:17:24
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               January 31, 2003, 01:15:03 ; Search time 2759 Seconds (without alignments) 3987.264 Million cell updates/sec
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378
1 tacggctgcttaagacgact.....taccattggagaaccatgcg 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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ALIGNMENTS

AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX245292	RESULT 1
Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Sudduth-Klinger, J., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M.,	Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 378)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.		AX245292.1 GI:15859966	AX245292	Sequence 222 from Patent WO0166753.	AX245292 378 bp DNA linear PAT 28-SEP-2001		

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KEYWORDS
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Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M. Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
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Patent: WO 0166753-A 222 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
Location/Qualifiers
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Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Crain,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 278; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 GAATGACGCAGCAGCTCTGAGAGGAACATAAGGAAAACACCCAAGCCGGAGTCTCTCACA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 GAATGACGCAGCGGCTCTTAGAGGAACATATGGAAAACACCCAAGCCGGAGTCTCTCACA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGC 313
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Patent: WO 0166753-A 300 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 318)
Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Kilnger,J., Reinhard,C., Randazzo,F., Kennedy,G.C.,
Kossam,A., Lamson,G., Dimanac,R., Crkvenjakov,R., Dickson,M.
Dimanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
                                                                                                                                                                                                                          Human DNA sequence from clone RP1 STSs and GSSs, complete sequence. AL135937
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1_to 59231)
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1 (bases 1 to 318)
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                              59231 bp DNA linear rotation clone RP1-278022 on chromosome 20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20 IMPORTANT: This sequence is not the entire insert of clone RP1-278022 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-697P8 is at 100 in this sequence. The true right end of clone RP4-1099D15 is at 100 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality -30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP1-278022 is from the later of the form of the for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Mar 15, 2000 this sequence version replaced gi:7242336. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wit only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VECTOR: PCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the library RPCI-1 constructed by the group of Pieter de Jong. For
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2927.
                                                                            /note="13 copies 2 mer aa 96% conserved"
complement(10684. .11081)
                                                                                                                                                                                                                                                        8546.
                                                                                                                                                                                                                                                                                                                                                                                                                 complement(5199
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complement(5199. .5709)
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/db_xref="taxon:9606"
/chromosome="20"
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                                            note="match: GSS: Em:AQ662878"
                                                                                                                                                                                                                       /note="L1MC4 repeat: matches 7117. .7739 of consensus"
                                                                                                                                                                                                                                                                                                                                    /note="Charlie4a repeat: matches 25.
                                                                                                                                                                                                                                                                                                                                                                     7115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1ME2 repeat: matches 5541.
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                                                                                                                                                               'note="AluSq repeat: matches 1. .225 of consensus"
                                                                                                                                                                                                                                                                            'note="MIR repeat: matches 13. .81 of consensus"
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complement(15295. .15803)
/note="match: GSS: Em:AQ754141"
/note="AluY repeat: matches 1. .309 of consensus"
31750. .32046
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/note="L1MA9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (19364
                                                                                            note="MER1B repeat: matches 1.
                                                                                                                 /note="L2 repeat: matches 2124.
30877. .31223
                                                                                                                                                                      /note="LlMC4 repeat: matches 7430. .7849 of consensus"
                                                                                                                                                                                                          /note="56 copies 2 mer ta 73%
                                                                                                                                                                                                                                       /note="LIMC4 repeat: matches 7841. .7973 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L1M1 repeat: matches 5678. .5763 of consensus"
25134. .25443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="LTR16C repeat: matches 1. .387 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-"match: GSS: Em:AQ694331"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"L2 repeat: matches 2657.
                                                                                                                                                                                                                                                                                                                                        e="AluSq repeat: matches 1.
)5. .26579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :e="34 copies 2 mer ga 79% conserved"
>lement(19364. .19600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em "MIR repeat: matches 50. .139 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9. .13813
e-"L2 repeat: matches 2195. .2293 of
4. .14087
                                                                                                                                                                                                                                                                                                                   e="L1MC/D repeat: matches 5290. .5579 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                            e-"AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e="match: GSS: Em:AQ035738"
2. .22242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e="MIR repeat: matches 24. .50 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e="MER58B repeat: matches 2. .341 of consensus"
1. .18717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="MIR repeat: matches 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .e="match: GSS: Em:AQ035618"
?7. .13423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e-"AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="L1ME3A repeat: matches 5427.
9. .16808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ="L1ME3A repeat: matches 5964. .6159 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="L1MA5_repeat: matches 6025.
                                                                                                                                                                                                                                                                              "MIR repeat: matches 20. .142 of consensus"
                                  "L2 repeat: matches 1945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .18952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      copies 2 mer ta 68% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 410. .521 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 1.
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                                                                                            . 337
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                                                  .2124 of consensus"
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44765. .44818
/note="MIR repeat: matches 200.
complement(45503. .46337)
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/note="MSTB repeat: matches 1.
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complement(43484. .44004)
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40380. .40675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32189. .32474
/note="AluJo repeat: matches 1.
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                                                                                                                                                                                                                                                                                                      /note="L1MA9 repeat: matches 4226.
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40676. .42726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L2 repeat: matches 1809.
                                                                                                                                                                                                                                                                                                                                                                                                 19992. .40126
"note-"AluJo repeat: matches 2. .134 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="LIM3d repeat: matches 251. .280 of consensus" 19314. .39717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note-"MIR repeat: matches 191.
15160..35351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MIR repeat: matches 84. .150 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7904. .37941
note="19 copies 2
                                                                                                                                                                                                                                                                                                                                                                                                                                   note="LlMA9 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MIR repeat: matches 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="LlM3e repeat: matches -879. .779 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER5A repeat: matches 7.
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                                                                                                                                           31.5%; Score 119; DB 9; 100.0%; Pred. No. 5.3e-25;
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                                                                                                                                                           Length 59231;
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ACCESSION VERSION KEYWORDS RESULT 6 AC119775/c REFERENCE SOURCE DEFINITION Locus AUTHORS ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; (
Mammalia; Eutheria; ! 162394 bp DNA Rattus norvegicus clone CH230-464J18, *
***, 61 unordered pieces.
AC119775 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., AC119775 AC119775.4 GI:21747184 Rattus. HTG; HTGS_PHASE1. (bases 1 to 162394) Chordata; Rodentia; Craniata; Vertebrata; Sciurognathi; Muridae; ·linear | Euteleostom1;
; Murinae; HTG 18-JUL-2002 IN PROGRESS

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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REFERENCE
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2 (bases 1 to 162394)

2 (bases 1 to 162394)

Worley,K.C.

Direct Submission

Submitted (02-MAY-2002) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 162394)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:20467838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                               Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 10
Assembly program: Phrap; version 0.99
Consensus quality: 104933 bases at le
Consensus quality: 112584 bases at le
Consensus quality: 117408 bases at le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: GVQM
Center clone name: CH230-464J18
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least Q30
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Mouse DNA
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 28, 2002 this sequence version replaced gi:21531387.
                                   Submitted (27-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                        Dunn, M.
                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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148 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 207
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This sequence was finished as follows unless otherwise noted: all regions with described as follows unless otherwise noted: all
                                                                                                                Submitted (04-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zface@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 176543)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unordered pieces. AL845312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALB45312 176543 bp Danio rerio clone DKEY-287F10, ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The lowing abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
                                                             Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                 zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL845312.1 GI:22205007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-173012 is from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               constructed by the group of Pleter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VECTOR: pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62140
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                                   code:
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/clone_lib="RPCI-23"
46575 c 46966 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .223604
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http://www.sanger.ac.uk
                                                                                              -- Genome Center
                                      ဗ္ပ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [-23"
5 g 67923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA linear HTG 09-AUG-2002 SEQUENCING IN PROGRESS ***, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                     Vertebrata; E
Ostariophysi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ب</u>
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REFERENCE AUTHORS

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BASE COUNT
ORIGIN
                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
AC129650
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                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20135 TGGACGTGTTCAACATGCAATAAATGTGGATAAGACCAATGAAGCACTTTTTGAAGGC 20076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 AGAAGTCTTCTTGGCAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 TGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGTGATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTGTTTCATTTTAA 19999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTTTCAGTATAAAACAATTAGTCGCATCACAAGGCTCTCCAAAGTTTCATGCAATTTC 20016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator; 100% of reads CACONSENBUS QUALITY: 175506 bases at least QAO CONSENBUS QUALITY: 17559 bases at least QAO CONSENBUS QUALITY: 176033 bases at least QAO Insert size: 176343; sum-of-contigs Insert size: 176343; sum-of-conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: zK287F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coverage: 10.57x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: zface@sanger.ac.uk
                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-9H1, 67 unordered pieces. AC129650
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                             HTG; HTGS_PHASE1.
Norway rat.
                                                                                                                                                                                                                                                                                                                                                       AC129650
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                                                                                                                                                                                             AC129650.1 GI:22024419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57205
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/note="assembly_fragment:02085
fragment_chain:1"
166620 .176543
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1. .176543
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Danio rerio"
/db_xref="taxon:7955"
/clone-"DKEY-287F10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- Summary Statistics
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165519: contig of 96228 bp in length
16519: config of 96228 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       embly_fragment:01906.0"
31568 g 55615 t 20
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                                                                                                                                                                                                                                                                                                                                                       176030 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
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                                                                                                                                                                                                                                                                                                              linear HTG 31-JUL-2002 SEQUENCING IN PROGRESS ***,
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TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

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Bouck, J., Bowie, S., Brieva, M., Brown, R., Brown, N., Brydt, N., Bowie, S., Burch, P., Brown, M., Brydt, N.C., Chargo, C., Chargo, C., Chargo, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chargo, S.R., David, R., David, R., David, R., David, R., David, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., David, R., Delaney, K.R., David, R., Delanet, C.C., Elhaj, C., Escotto, M., Earlis, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garnet, T., Garza, M., Gill, R., Garlis, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garnet, T., Garza, M., Gill, R., Gao, J., Garcia, A., Garnet, T., Garza, M., Gill, R., Garzi, M., Gill, R., Garzi, M., Harris, C., Karlyk, J., Harris, K., Harris, M., Garzi, M., Karlyk, J., Luch, M., Halles, S., Joudhi, S., Karlyk, J., Luch, M., Loulseyed, H., Lozado, R., Martinez, E., Mahsen, J., Martinez, E., Mahsen, J., Martinez, E., Mahsen, M., Martinez, E., Mahsen, J., Martinez, E., Mahsen, M., Rui, Y., Pace, A., Payton, B., Peery, J., Perez, L., Perez, L., Perez, J., Path, M., Rui, Y., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu,C., Wu,Y., Wu,Y.F., Zh
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 115101 bases at least Q40
Consensus quality: 125022 bases at least Q20
Consensus quality: 125022 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: GDLF
Center clone name: CH230-9H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine Center code: BCM
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1356

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This record will as soon as it is be preserved.
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1072
1244
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39721
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31770
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2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medical Center Dr., R
3 (bases 1 to 91071)
Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 91071)
Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Spriggs, T.A., Mason, T.M., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin,x.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 91071)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAVLTSEGALFLEDQDLMRPVWSVFGEDHNDTVKFRFLRLDRDGNLRWSWNEDSRIW
KPVWQAVENQCRVFATCGSQVCSFNSSGYTECRCPFNARVSVSVSDPKCLVPPQKPGKSK
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TRYISGYSDPSLSSISYVKTCLDPIAVDPNNVSKESPVTVTKSHSICIPCLVGATSTT
LVLFLGFQLGIVYYIYRRKKLAKKKAERFSKATNPKGVMIFSVDEIKAMTDNDNDND
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QKFPAFEMLRAASENGRSSYYSLHLEDSGRLELRWESNITFWSSGNEVVKKKKKKKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPOIFKGVMEENELVAVKEVEATLTEEBRKFRSSASKICTMHKKULANLEGYCCELGRR
FLYYEYAKNGSILDHIVDPLRSKKTTWRIRTDTCLSVAKALCYLHMECREFVSHGNLN
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3927. .4062,4153. .4274,4362. .4724,4801. .4930,5029.
5183. .5296,5446. .5500,5725. .5857))
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                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3329. .5857)
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184. .2478
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3927. .4062,4153. .4274,4362. .4724,4801. .4930,5029.
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GGRKETVVDKGLEGCFDVEELERVLRISFWCVQTDERLRPSWGEVVKVLEGTLSVDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="overlap with BAC clone T6D20
(U90439:82778. .95824)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPPFACARSSPTNSSESSQSLYEP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene-"At2g41890"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"At2g41890"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'clone="T11A7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         map-"CIC11C08"
                    /product="putative guanylate kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family-"(GAA)n"
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translation-"MGEAPAVLVDHPENGHSNGVCVKSEPENTEITVDVGDRIFLIGG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis
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repeat_region
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FPSMFGFSVSHTTRSPRSMEMGVHYHFADKKYMEKEIKDKFLEFASVHGNLYGTSI
ESVEAVTDSGKRCILDIDUOGARSVEASSLDAIFIFVCPSUKELEDBLRARGCTETEE
QIQKRLRNAEAEIKEGISSGIFGLILYNDNLEECYKKLKNLLGLDGLAHVNGVEIEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGNCCGTAGSLIQDKQKKGFKLPNPFSNEYGNHHDGLKLIVLKE
PTGHEIKOKYKLGRELGRGEFGVTYLCTEIETGEIFACKSILKKLTYSIDIEDVKRE
PTGHEIKOKYKLGRELGRGEFGVTYLCTEIETGEIFACKSILKKLTSIDIEDVKRE
VEIMROMPEHFNIVTLKETYEDDKAVHLYMELCEGGELFDRIVARGHYTERAAASVIK
TIIEVVOMCHKHGVMHDDLKPENFLPANKKETASLKALDGGLSVETKKPERENEIVGS
PYYMAPEVLRESYGQEIDIWSAGVILYILLCGVPPFWAETEHGVAKAILKSVIDFKRD
PAPKYSDNAKDLIKKMLHPDFRRRLTAQOVLDHPWIONGKNASUVSLGETVRARLKQF
SVMNKLKKRALRVIAEHLSVEETSCIKERFOVDDTSNRGKITITELGIGLOKLGIVV
PODDIQILMDAGGDVDKGGYLDVNEFVAISVHIRKGNDEHLKKAFTFFDKNKSGYIEIVE
ELRDALADDVDTTSEEVVEAIILDVDTNKDGKISYDEFATMMKTGTDWRKASRQYSRD
LFKCLSLKLMQDGSLQSNGDTK
LFKCLSLKLMQDGSLQSNGDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7944..7980)
/rpt_family="(GAA)n"
join(8017..8640,9217..9417)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THERNNESIGVQIYDKISNNWESPIVLGTGPKPSKGYSAEVLEQGRILVIKKGSPRND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(10329...10
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mltlyHqerspdatsndrdetpetvvrevhaltpapednsrtmt
atlppppafrgyfspprsattmsegenfttisrefnalviagssmennelmtrdytqr
ederqdelmrihedtdheeetnplaivpdqypgsgldpgsdngpgqsrvgstvqrvkr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLPIEYAVSKMEDKIIIQETGKETRNKIVVDISSLNGGAPGRTRGILVDAIKF*
                                                                                                                                                                                                                                                                                                                                                                                                      complement(15877. .15 /rpt_family="AT_rich" 16477. .18618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(8642. .8664)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mektonnvakaorkaeerrataeakrgtevakvvevanimralgrppakrsffsfs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eeveak i tawqtak lan i nnrfkredav i ngwf neqvnkanswmkk i erkleerkaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative DNA binding protein"
/protein_id="AAM14826.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(7600. .8640,9217. .9670)
/gene="At2g41870"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="At2g41870"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative calcium-dependent protein kinase"
/protein_id="AAM14824.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(<10750. .11250,11362. .11485,11563. .11706,11798. .11950,
12044. .12327,12415. .12645,12735. .>12890)
/gene="_ht2941860"
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17823. .17904,17999. .18107,18206. .18319,18409. .>18618)
//gene="Att2941850"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (14214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="At2g41860"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )oin(10750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"T11A7.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="At2g41860"
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/note="T11A7.5"
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                                                                                                                                                                                                                         oin(16477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _family-"AT_rich"
                                                                                                                                                                                                 .17904,17999. .18107,18206. .18319,18409. .18618)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .15901)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14243)
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CDS

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ACCESSION
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AC104652
LOCUS
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                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                      41484 GGAGACCATATATGGACTTCTGGAACTCCGCTTAACATATCTCTCGTGTACACACATGCG 41543
                                                                                                                                                                                                                                                                    41604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTT 165
                                                                                                                                                                                                                                                                                                                                                                                              166 CTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGAC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                  AGTTAAACGTAAAGCTTTATTAAACAAAGAACAAAT 41639
                                                                                                                                                                                                                                                                                                              TGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT 261
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                        Homo sapiens BAC
AC104652 AC034273
AC104652.3 GI:18
                                                                                                                                                           AC104652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25475. .2558,35660. .25707,25758. .28971,26076. .26241,26613. .268905,27234. .27749,27973. .281122,28266. .28341,28553. .28680,28855. .29049,29166. .29303,29391. .29501,29600. .29839,29941. .>30105)

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/5475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="(A)n"
18645. 18742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIVLDRVNIKGGKATCTNANVVDKGAVLPQCNST"
complement(17300...17333)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLVPKGNTYLLKSIQLTGPCNSILTYQIFGTLSASQKRSDYKDISKWIMFDGYUNLSV
DGGDTGVVDGNGETWRQNSCKRKAKALTFYNBKSLTYNKIKVRNAQQIQISIEKCSN
VQVSNVVDGNGETWRQNSCKRINTONIRVSBSILTGRDDCISIESGSQNVQINDINDTC
GPGHGISIGSLGDDNSKAFVSGVTVDGAKLSGTDNGVBIKTYQGGSGTASNIIFQNIQ
MDNVKNPIIIDQDYCDKSKCTTEKSAVQVKNVYYRDISGTSASENAITFNCSKNYPCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGRASEEEKWVPVTKLGRLVAAGHIKQIEQIYLHSLPVKEYQIIDMLIGPTLKDEVMK
IMPVQKQTRAGQRTREKAFVVVGDGNGHVGLGVKCSKEVATAIRGAIILAKLSVVPVR
RGYWGNKIGKPHTVPCKVTGKCGSVTVRMVPAPRGSGIVAARVPKKVLQFAGIDDVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(24083...24229,24605...24679,24862...24986,25189...25303,
25475...25558,25660...25707,25758...25871,26076...26241,
26613...26905,27234...27749,27973...28122,28266...28341,
28553...28680,28855...29049,29166...29303,29391...29501,
29500...29839,29941...30105)
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/note="T11A7.7; predicted by genscan; similar to
2191175 AF007270"
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/gene="At2g41840"
/codon_start=1
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/note="T11A7.6; supported by full length cDNA:
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                                                                                                                                                                                                                                                                                                                    Submitted (21-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Feb 1, 2002 this sequence version replaced gi:18087701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-FEB-2002) Genome
University School of Medicine,
MO 63108, USA
5 (bases 1 to 130206)
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Direct Submission
Submitted (18-DEC-2001) Genome Sequencing Center, Washington Center, Washingt
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1 (bases 1 to 130206)
Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
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Waterston, R.H.
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The sequence of Homo sapiens
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Drafting Center: WIBR
                                      Center project name: H_NH0273F23
                                                                                                                                  Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
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s BAC clone RP11-273F23
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NOTICE: NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

SOURCE INFORMATION:

망 ð 밁 Ş 밁 Ş

The RPCI-11 human BAC library was made from the blood of one donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenc Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.chori.org pBACe3.6 fone male Frengen, E., from

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-679C8, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-273F23; actual end is at base position 61045 of RP11-679C8.

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FEATURES
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          /rpt_family="ERV1" 24408. .25160
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22477 . . 22755
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/db_xref="taxon:9606"
/chromosome="4"
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23577. .23811
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7. .17679
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9. .23213
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AC108866
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                                                                                           152822 bp DNA
Homo sapiens BAC clone RP11-44D21 from
AC108866
AC108866.5 GI:19848440
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66; Conser
 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 152822) Sulston, J.E. and Waterston, R.
                                                                          Homo sapiens.
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ilarity 58.9%;
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34315. .34356
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25351. .25487
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34982. .35058
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7. .30735
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Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (30-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-APR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Mar 30, 2002 this sequence version replaced g1:19570183.
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NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-44D21;
actual end is at base position 152822 of RP11-44D21.
                                                                                                          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                   MAPPING INFORMATION:
MAPPING INFORMATION for this clone was provided by Dr. John D. Mapping information for this clone was provided by Dr. John D. McPharson, Department of Genetics, Washington University, St. MCP For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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31674. .32256
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             1 (bases 1 to 190912)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 10, clone RP11-435B15
Unpublished
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 184508 bases at least Q40 consensus quality: 187307 bases at least Q30 consensus quality: 188400 bases at least Q20 Insert size: 198000; agarose-fp Insert size: 19812; sum-of-contiss Quality coverage: 4.9 in Q20 bases; agarose-fp Quality coverage: 5.1 in Q20 bases; sum-of-contiss

Sequencing vector: Plasmid; n/a; 100% of reads

Center project name: L10588 Center clone name: 435_B_15

Contact: sequence_submissions@genome.wi.mit.edu

Center: Whitehead Institute/ MIT Center code: WIBR Web site: http://www-seq.wi.mit.edu

Center for Genome

Research

-- Genome Center

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CE 2 (bases 1 to 190912)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Chepel, V., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferrelta, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferrelta, P., Dearellano, K., Dewar, K., Diaz, J.S., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Jones, C., Kann, L., Karattas, A., Lancoque, K., Limezares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marguits, N., McCarthy, M., McEwan, P., McKernan, K., McCharthy, M., McEwan, P., McKernan, K., McCharthy, M., McEwan, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thomann, N., Stolauer, S., Severy, P., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tilsen, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
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SUBMITTED (19912)

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Biren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,

Barna, N., Bastlen, V., Boguslavkly, L., Boukhgalter, B., Brown, A.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Collymore, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,

Bodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,

Gardyna, S., Ginde, S., Goyette, W., Graham, L., Grand-Pierre, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, W., Illey, I., Johnson, R.,

Hagos, B., Heaford, A., LaRocque, K., Lamazares, R., Landers, T.,

Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,

Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McBernan, K.,

McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,

Murphy, T., Naylor, J., Nguyen, C., Norbu, P., McRernan, P., McRernan, R.,

Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,

Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,

Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,

Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,

Northert Submission.
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 14, 2001 this sequence version replaced gi:10334889. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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8805 8904: gap of 100 bp
8905 9991: contig of 1087 bp in length
9992 10091: gap of 100 bp
10092 11974: contig of 1883 bp in length
11975 12074: gap of 100 bp
12075 14089: contig of 2015 bp in length
14090 14189: gap of 100 bp
14190 15697: contig of 1508 bp in length
1598 18961: gap of 100 bp
15862 18961: gap of 100 bp
16862 18961: gap of 100 bp
1798 18861: gap of 100 bp
18862 18961: gap of 100 bp
18862 18961: gap of 100 bp
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28884. .33590
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/db_xref="taxon:9606"
/chromosome="10"
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/clone_11b="RPCI-11 Human
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23839: contig of 2068 bp in lo
3939: gap of 100 bp
28783: contig 100 bp
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1227: gap of 100 bp
136743: contig of 46516 bp in
36843: gap of 100 bp
173143: contig of 36300 bp in
73243: gap of 100 bp
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90127: contig of 13210 bp in length
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21671: contig of 2710 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30960 bp DNA Caenorhabditis elegans cosmid Y46C8AL, AC024785
                                                                                                                                                                                            3 (bases 1 to 30960)
Waterston, R.H.
Direct Submission
Submitted (01-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
        Direct Submission
Submitted (28-JUN-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                Direct Submission
Submitted (28-MAR-2000)
University, 4444 Forest
5 (bases 1 to 30960)
                                                                                                                                                                                                                                                                        The sequence of C. elegans cosmid Y46C8AL Unpublished (2001)
                                                                                                                                                                                                                                                                                                             Cordes, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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Louis, MO 63110, USA
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42375..51118
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173244. .190912
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51219. .63841
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53942. .76817
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Pred. No. 1.
                                                                                                   Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of vujl Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFecome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from Blastx analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Aver Louis, MO 63110, USA Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analysis see:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For a graphical representation of this cosmid sequence and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        more than one ml3 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neighboring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         once,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.wormbase.org/db/seq/sequence?name=Y46C8AL;class=Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    It may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 30960)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   þ 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y be shorter because we only sequence overlapping sections or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Genetics, Washington University St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cosmid is F56D6, 200 bp overlap; the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence may not be the entire insert of this clone.
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(protein id="AAF60598.1"
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ARNWCHYKNPVGSSYLAYVPDQKTSNYLAFYARTAFGFAAQHFWIGLSKNGSSGSLTW
DNGSPVGYTNLGSQNGNNLYFTESLANTKWNTLGDDKINYFVCSYNPATTPTTPSTTT
                                                                                                                                                                                                                                                                                                                                                           ss=Sequence"
                                                                                                                                                                                                                            'gene-"Y46C8AL.3"
                                                                                                                                                                                                                                                                                           ]oin(1479. .1698,2460. .2723,2768. .2836,2897. .2951,
3004. .3097,4144. .4383,4441. .4585,4636. .4733,4784. .4905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="Y46C8AL.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:6239"
/chromosome="IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'strain-"Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=Y46C8AL.3;cla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one-"Y46C8AL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEIGHBORING COSMID INFORMATION
                                                                                                                                                                                                                                                                    .4984)
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/protein_id="AAF60602.1"
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PYTYQNTESNSILYKQQYTEAI IREDTRQPOSIMYENDYNOALAYVRNHLPDYKLGFQ
ESTTGSDVLDY INNEY NNSSACASYVMYLSKRY PNTPDISRTVAKYRQYHGIVNFLAS
NYPEGGSQSQYLFDLASQTNGLYG IEODSLESKRILYMPLRTRYFIYAVNAKYSGEGE
QYLPPMSYPQEDDFLIMYSYQSHLPYSNYQYVNLKMYNPSFPYSDKFEMQPYYMDSNT
NYNTLTIGLSQNYXNMTIDYLTYTNTDYETMQIRLYSSYFTNYMLPYSN*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TADKNCQPGGQQTVLFAYSNDLDPISRFDLRQPEDIGYFTDYDNVTDYVDSHAPDSSL
GFGDTKTGSNVLDVIDKFYDNTKLTPCGSIVMVLLKRYSNSNDISNIVAKVRKHHGSV
NFIASNTPSGGTNSRVLFDLSSRTNGLYVIDRDSYFMQSIDMMFLIERYPIYAANPVV
16234. .21008
/gene="Y46C8AL.6"
                                                                                                          MTIDYIYTNTDVETMQIRFYSSL"
                                                                                                                                                               YNDISSCGSVVMVLSKRYPNTMDISSTVAKVRQYHGMVNFLASNAPSGGTQSRVLFDL
SSRTNGIYSIEEDATFLHFIGWMPLRERYPIYAVNVKVSGHGSQVLPPMSVPRDVTYL
IMVSLQSHLPISNVQSAKLNWFNPPPPQGALSWQPSEWAYTNSNSGGNRRIIDPAVYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name-Y46C8AL.5;cla
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NELFVCYHENMCIISQVLSECKLKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSDYSDYHEVYSNYSDYSDYHEVYSNYSDYSDYHEVTNYSDYSDYHEVYTNY
HEVYSNYSDYHEVYSNYSDYSDYHEVYSNYSDYHEVTTNYSDYSDYHEVYTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(8898. .9932,10290. .10334))
/gene="Y46C8AL.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Y46C8AL.2"
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AFYARSAFGQSAESFWIGLSRNGSSGSLSWDNGFPVIYTNFGSKVGNNYFTEKISNSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=Y46C8AL.4;cla
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WNNPYTNANGKRANLDASGFAMTVEYVYNDSGDHPMQIRFYSPEATDFWLPYTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(12224. .12333,12381. .12503,12615. .12780,1:
13870. .14145,14204. .14387,14441. .14534,15204.
15486. .15630,15678. .15772,15826. .15951)
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/protein_id="AAF60597.1"
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/translation-"MRAEISYPRSAFASFNFQHLFSLFSLFQLFSMILKLCLLATLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8637.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Y46C8AL.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="Y46C8AL.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="Y46C8AL.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation-"MTYDDAHNWCHFKNPVGNKANAKYNEVYTDYSDYHQVYSDYSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'codon_start≖l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="Y46C8AL.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"for a graphical representation of this
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7159,7390. .7623,8127. .8271,8322. .8416,8469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .12780,13562. .13778,
34,15204. .15437,
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/note="for a graphical representation of this gene see: http://www.wormbase.org/db/seq/sequence?name=Y46C8AL.6;cla

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REFERENCE
AUTHORS
TITLE
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AL732628/c
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VERSION
KEYWORDS
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DEFINITION
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ORGANISM
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 AATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 CATGCTTTGACTGTTGAAAAGAGACCTTTGG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTICCACTGTACGTTAAAATATATACTTACATGCCAAGTAGTTGCTTGTTTTTTGATCAG 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 174196)
                                                                                                                                                      Assembly program: XGAPA; Version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 17355 bases at least Q40
Consensus quality: 173741 bases at least Q30
Consensus quality: 173854 bases at least Q20
Consensus quality: 173854 bases at least Q20
Insert size: 173996; sum-of-contigs
Insert size: 161892; 19.9% error; agarose-fp
Quality coverage: 6.72x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zface@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug.11, 2002 this sequence version replaced gi:21911655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL732628.8 GI:22204545
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                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: zC144F18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: zface@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
                                                                                                                                           coverage: 7.22x in Q20 bases; agarose-fp
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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rerio clone CH211-144F18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- Genome Center
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RVFQVKVGDSLSSFKKADCGYPQGAVLSPLLFGIFVNEIPHILPPALKCGPADDKK
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YTAIPSNSNNNVHLQKAIETIVEMSKATKLALNNDKTVCISLGRNTTEFGYTENSLI
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join(16234. .16362,17175. .17391,17491. .17739,18508. .19286,
19338. .19628,20472. .20616,20666. .20763,20809. .20930,
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/gene="Y46C8AL.6"
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63.7%;
                                                                                                                                                                                                                                                                                                                                                                                        Summary Statistics
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Pred. No. 1.5;
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Job time : 3850 secs

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ORIGIN
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Best Local Similarity
Matches 75; Conserv
                                                                                                                                      98366 TGGACGTGTGTTCAACATGCAATAAATGTGGATAAGACCAAGGAAGCACTTTTTGAAGGC 98307
                                                                    98306
 98246
                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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                                   320
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                                                                                                                                                                         200 TGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGG 259
GGGTGTTTTATTTTTAA 98230
                                                                   AAGTTCCAGTATAAAACAATTAGTCGCATCCCCAGGCTCTCCAAAGTTTCATGCAATTTC 98247
                                                                                                    ATGGTGATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGC 319
                                 AGAAGTCTTCTTGGCAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number wil
be preserved.
                                                                                                                                                                                                                                                                                                59260 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53762 53861: gap of 100 bp
53862 77324: contig of 23463
77325 77424: gap of 100 bp
77425 174196: contig of 96772
Location/Qualifiers
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment:01503
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77425...174196
                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:00262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment:00869
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